



# SEQUENCE LISTING

<110> Wonderling, Ramani S.  
Boroughs, Karen L.

<120> CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES  
THEREOF

<130> IM-5

<140> 09/917,265

<141> 2001-07-27

<150> 60/223,016

<151> 2000-08-04

<160> 111

<170> PatentIn version 3.2

<210> 1

<211> 514

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (114)..(512)

<220>

<221> misc\_feature

<222> (470)..(470)

<223> n = unknown at position 470

Xaa = unknown at position 119

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aaaccttcca gatcccttcc tctcttagga aactattgag cacagggata aag atg 116  
Met  
1

act gct ata cca gta gat gat tgc atc aac ttt gtg gga atg aaa ttt 164  
Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys Phe  
5 10 15

att gac aat aca ctt tac ttt gta gct gac agt gat gaa aac ctg gaa 212  
Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu Glu  
20 25 30

aca gat tac ttt ggc aag ctt gaa cat aaa ctc tca atc tta cga aac 260  
Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn  
35 40 45

ttg aac gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt 308  
Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe

50	55	60	65	
gag gat atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa				356
Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu				
	70	75	80	
ttt atc ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta				404
Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val				
	85	90	95	
acc atc tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac				452
Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn				
	100	105	110	
aaa att att tcc ttt aan gga atg agt cct cct gag agt atc aat gat				500
Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn Asp				
	115	120	125	
gaa gga aat gac at				514
Glu Gly Asn Asp				
130				

<210> 2  
 <211> 133  
 <212> PRT  
 <213> Felis catus

<220>  
 <221> misc\_feature  
 <222> (119)..(119)  
 <223> The 'Xaa' at location 119 stands for Lys, or Asn.

<400> 2

Met Thr Ala Ile Pro Val Asp Asp Cys Ile Asn Phe Val Gly Met Lys
1 5 10 15

Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala Asp Ser Asp Glu Asn Leu
20 25 30

Glu Thr Asp Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg
35 40 45

Asn Leu Asn Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val
50 55 60

Phe Glu Asp Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr
65 70 75 80

Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala
85 90 95

Val Thr Ile Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu  
 100 105 110

Asn Lys Ile Ile Ser Phe Xaa Gly Met Ser Pro Pro Glu Ser Ile Asn  
 115 120 125

Asp Glu Gly Asn Asp  
 130

<210> 3  
 <211> 514  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> misc\_feature  
 <222> (45)..(45)  
 <223> n = unknown at position 45

<400> 3  
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 ttgttctcac aggagagagt agacatgggc ttataattca cagagatggg tactgccaga 120  
 cctctagtga ggctatcttt atacatatat atgataaatt cagtccgggg tgcattatct 180  
 gtacagtcag aatcaggcatt atcctcaaac acaggttgat ctccctgggt aatgaagaga 240  
 acttggtcgt tcaagtttcg taagattgag agtttatggt caagcttgcc aaagtaatct 300  
 gtttccaggt tttcatcact gtcagctaca aagtaaagtg tattgtcaat aaatttcatt 360  
 cccacaaagt tgatgcaatc atctactggg atagcagtca tctttatccc tgtgctcaat 420  
 agtttctctaa gagaggaagg gatctggaag gtttgagggc cctttctttt cctgagctgt 480  
 gtagatggca gaaggtggca ggagcgcctt tagc 514

<210> 4  
 <211> 502  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (3)..(464)

<220>  
 <221> misc\_feature

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<222> (126)..(126)
<223> n = unknown at position 126
Xaa = unknown at position 42

<400> 4
gc aag ctt gaa cat aaa ctc tca atc tta cga aac ttg aac gac caa      47
  Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln
    1             5             10             15

gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat atg cct      95
Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro
      20             25             30

gat tct gac tgt aca gat aat gca ccc cgg nct gaa ttt atc ata tat      143
Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr
      35             40             45

atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc tct gtg      191
Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val
      50             55             60

aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att att tcc      239
Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser
      65             70             75

ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga aat gac      287
Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp
      80             85             90             95

atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag ata caa      335
Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln
      100            105            110

ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa aaa gag      383
Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu
      115            120            125

aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat ggg gat      431
Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
      130            135            140

aag tcc ata atg ttc act gtt caa aac aag aat tagatattaa aattgcataa      484
Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn
      145            150

tttgaaaaaa aaaaaaaa      502

<210> 5
<211> 154
<212> PRT
<213> Felis catus

<220>
<221> misc_feature
<222> (42)..(42)
<223> The 'Xaa' at location 42 stands for Thr, Ala, Pro, or Ser.

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<400> 5

Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val  
1 5 10 15

Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp  
20 25 30

Ser Asp Cys Thr Asp Asn Ala Pro Arg Xaa Glu Phe Ile Ile Tyr Met  
35 40 45

Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn  
50 55 60

Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile Ile Ser Phe  
65 70 75 80

Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly Asn Asp Ile  
85 90 95

Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys Ile Gln Phe  
100 105 110

Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu Lys Glu Lys  
115 120 125

Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys  
130 135 140

Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
145 150

<210> 6

<211> 502

<212> DNA

<213> Felis catus

<220>

<221> misc\_feature

<222> (377)..(377)

<223> n = unknown at position 377

<400> 6

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attatggact tatccccatt ttcattccttt tttttcaaaa tgagtttgaa aagatctttc 120  
tctttttcac aagctagaaa gtacccttg tacaatgaag actcaaattg tatcttatca 180  
tcatgtcctg gaacacttct ctgaaagaat atgatgtcat ttccttcac attgatactc 240  
tcaggaggac tcatttcctt aaaggaaata attttggttct cacaggagag agtagacatg 300  
gtcttataat tcacagagat gggtactgcc agacctctag tgaggctatc tttatacata 360  
tatatgataa attcagnccg ggggtgcatta tctgtacagt cagaatcagg catatcctca 420  
aacacagggt gatctccctg gttaatgaag agaacttggc cgttcaagtt tcgtaagatt 480  
gagagtttat gttcaagctt gc 502

<210> 7  
<211> 607  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
<222> (24) .. (599)

<400> 7  
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Met Thr Ala Ile Pro Val Asp Asp Cys Ile  
1 5 10  
aac ttt gtg gga atg aaa ttt att gac aat aca ctt tac ttt gta gct 101  
Asn Phe Val Gly Met Lys Phe Ile Asp Asn Thr Leu Tyr Phe Val Ala  
15 20 25  
gac agt gat gaa aac ctg gaa aca gat tac ttt ggc aag ctt gaa cat 149  
Asp Ser Asp Glu Asn Leu Glu Thr Asp Tyr Phe Gly Lys Leu Glu His  
30 35 40  
aaa ctc tca atc tta cga aac ttg aac gac caa gtt ctc ttc att aac 197  
Lys Leu Ser Ile Leu Arg Asn Leu Asn Asp Gln Val Leu Phe Ile Asn  
45 50 55  
cag gga gat caa cct gtg ttt gag gat atg cct gat tct gac tgt aca 245  
Gln Gly Asp Gln Pro Val Phe Glu Asp Met Pro Asp Ser Asp Cys Thr  
60 65 70  
gat aat gca ccc cgg act gaa ttt atc ata tat atg tat aaa gat agc 293  
Asp Asn Ala Pro Arg Thr Glu Phe Ile Ile Tyr Met Tyr Lys Asp Ser  
75 80 85 90  
ctc act aga ggt ctg gca gta acc atc tct gtg aat tat aag acc atg 341  
Leu Thr Arg Gly Leu Ala Val Thr Ile Ser Val Asn Tyr Lys Thr Met  
95 100 105  
tct act ctc tcc tgt gag aac aaa att att tcc ttt aag gaa atg agt 389

Ser	Thr	Leu	Ser	Cys	Glu	Asn	Lys	Ile	Ile	Ser	Phe	Lys	Glu	Met	Ser		
			110					115					120				
cct	cct	gag	agt	atc	aat	gat	gaa	gga	aat	gac	atc	ata	ttc	ttt	cag	437	
Pro	Pro	Glu	Ser	Ile	Asn	Asp	Glu	Gly	Asn	Asp	Ile	Ile	Phe	Phe	Gln		
		125					130				135						
aga	agt	gtt	cca	gga	cat	gat	gat	aag	ata	caa	ttt	gag	tct	tca	ttg	485	
Arg	Ser	Val	Pro	Gly	His	Asp	Asp	Lys	Ile	Gln	Phe	Glu	Ser	Ser	Leu		
	140					145				150							
tac	aag	ggg	tac	ttt	cta	gct	tgt	gaa	aaa	gag	aaa	gat	ctt	ttc	aaa	533	
Tyr	Lys	Gly	Tyr	Phe	Leu	Ala	Cys	Glu	Lys	Glu	Lys	Asp	Leu	Phe	Lys		
155					160					165					170		
ctc	att	ttg	aaa	aaa	aag	gat	gaa	aat	ggg	gat	aag	tcc	ata	atg	ttc	581	
Leu	Ile	Leu	Lys	Lys	Lys	Asp	Glu	Asn	Gly	Asp	Lys	Ser	Ile	Met	Phe		
				175					180					185			
act	gtt	caa	aac	aag	aat	tagatatt										607	
Thr	Val	Gln	Asn	Lys	Asn												
				190													
<210>	8																
<211>	192																
<212>	PRT																
<213>	Felis catus																
<400>	8																
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1				5				10						15			
Phe	Ile	Asp	Asn	Thr	Leu	Tyr	Phe	Val	Ala	Asp	Ser	Asp	Glu	Asn	Leu		
			20					25					30				
Glu	Thr	Asp	Tyr	Phe	Gly	Lys	Leu	Glu	His	Lys	Leu	Ser	Ile	Leu	Arg		
		35					40					45					
Asn	Leu	Asn	Asp	Gln	Val	Leu	Phe	Ile	Asn	Gln	Gly	Asp	Gln	Pro	Val		
	50					55					60						
Phe	Glu	Asp	Met	Pro	Asp	Ser	Asp	Cys	Thr	Asp	Asn	Ala	Pro	Arg	Thr		
65					70					75					80		
Glu	Phe	Ile	Ile	Tyr	Met	Tyr	Lys	Asp	Ser	Leu	Thr	Arg	Gly	Leu	Ala		
				85					90					95			
Val	Thr	Ile	Ser	Val	Asn	Tyr	Lys	Thr	Met	Ser	Thr	Leu	Ser	Cys	Glu		
			100					105						110			

Asn Lys Ile Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn  
115 120 125

Asp Glu Gly Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His  
130 135 140

Asp Asp Lys Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu  
145 150 155 160

Ala Cys Glu Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys  
165 170 175

Asp Glu Asn Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
180 185 190

<210> 9  
<211> 576  
<212> DNA  
<213> Felis catus

<400> 9  
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gaacataaac tctcaatctt acgaaacttg aacgaccaag ttctcttcat taaccaggga 180  
gatcaacctg tgtttgagga tatgcctgat tctgactgta cagataatgc accccggact 240  
gaatttatca tatatatgta taaagatagc ctactagag gtctggcagt aaccatctct 300  
gtgaattata agaccatgtc tactctctcc tgtgagaaca aaattatttc ctttaaggaa 360  
atgagtcctc ctgagagtat caatgatgaa ggaaatgaca tcatattctt tcagagaagt 420  
gttccaggac atgatgataa gatacaattt gagtcttcat tgtacaaggg gtactttcta 480  
gcttgtgaaa aagagaaaga tcttttcaaa ctcatTTtga aaaaaaagga tgaaaatggg 540  
gataagtcca taatgttcac tgttcaaaac aagaat 576

<210> 10  
<211> 607  
<212> DNA  
<213> Felis catus

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tacaatgaag actcaaattg tatcttatca tcatgtcctg gaacacttct ctgaaagaat	180
atgatgtcat ttccttcac attgatactc tcaggaggac tcatttcctt aaaggaaata	240
attttgttct cacaggagag agtagacatg gtcttataat tcacagagat gggttactgcc	300
agacctctag tgaggctatc tttatacata tatatgataa attcagtcctg ggggtgcatta	360
tctgtacagt cagaatcagg catatcctca aacacagggt gatctccctg gttaatgaag	420
agaacttggc cgttcaagtt tcgtaagatt gagagtttat gttcaagctt gccaaagtaa	480
tctgtttcca ggttttctac actgtcagct acaaagtaaa gtgtattgtc aataaatttc	540
attcccacaa agttgatgca atcatctact ggtatagcag tcattcttat ccctgtgctc	600
aatagtt	607

<210> 11  
 <211> 471  
 <212> DNA  
 <213> *Felis catus*

<220>  
 <221> CDS  
 <222> (1)..(471)

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gac caa gtt ctc ttc att aac cag gga gat caa cct gtg ttt gag gat Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp 20 25 30	96
atg cct gat tct gac tgt aca gat aat gca ccc cgg act gaa ttt atc Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile 35 40 45	144
ata tat atg tat aaa gat agc ctc act aga ggt ctg gca gta acc atc Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile 50 55 60	192
tct gtg aat tat aag acc atg tct act ctc tcc tgt gag aac aaa att Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile 65 70 75 80	240
att tcc ttt aag gaa atg agt cct cct gag agt atc aat gat gaa gga Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly 85 90 95	288
aat gac atc ata ttc ttt cag aga agt gtt cca gga cat gat gat aag	336

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys  
 100 105 110

ata caa ttt gag tct tca ttg tac aag ggg tac ttt cta gct tgt gaa 384  
 Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu  
 115 120 125

aaa gag aaa gat ctt ttc aaa ctc att ttg aaa aaa aag gat gaa aat 432  
 Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn  
 130 135 140

ggg gat aag tcc ata atg ttc act gtt caa aac aag aat 471  
 Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
 145 150 155

<210> 12  
 <211> 157  
 <212> PRT  
 <213> Felis catus

<400> 12

Tyr Phe Gly Lys Leu Glu His Lys Leu Ser Ile Leu Arg Asn Leu Asn  
 1 5 10 15

Asp Gln Val Leu Phe Ile Asn Gln Gly Asp Gln Pro Val Phe Glu Asp  
 20 25 30

Met Pro Asp Ser Asp Cys Thr Asp Asn Ala Pro Arg Thr Glu Phe Ile  
 35 40 45

Ile Tyr Met Tyr Lys Asp Ser Leu Thr Arg Gly Leu Ala Val Thr Ile  
 50 55 60

Ser Val Asn Tyr Lys Thr Met Ser Thr Leu Ser Cys Glu Asn Lys Ile  
 65 70 75 80

Ile Ser Phe Lys Glu Met Ser Pro Pro Glu Ser Ile Asn Asp Glu Gly  
 85 90 95

Asn Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asp Lys  
 100 105 110

Ile Gln Phe Glu Ser Ser Leu Tyr Lys Gly Tyr Phe Leu Ala Cys Glu  
 115 120 125

Lys Glu Lys Asp Leu Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn  
 130 135 140

Gly Asp Lys Ser Ile Met Phe Thr Val Gln Asn Lys Asn  
 145 150 155

<210> 13  
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 <213> Felis catus

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 agactcaaat tgtatcttat catcatgtcc tggaacactt ctctgaaaga atatgatgtc 180  
 atttccttca tcattgatac tctcaggagg actcatttcc ttaaaggaaa taattttggt 240  
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 agtgaggcta tctttataca tatatatgat aaattcagtc cggggtgcat tatctgtaca 360  
 gtcagaatca ggcatatcct caaacacagg ttgatctccc tggttaatga agagaacttg 420  
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<210> 14  
 <211> 1233  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(1230)

<400> 14  
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 Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Gln Phe Ile Asn Ser  
 1 5 10 15  
 gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa 96  
 Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys  
 20 25 30  
 aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct 144  
 Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala  
 35 40 45  
 acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa 192  
 Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys  
 50 55 60  
 ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac 240

Gly 65	Pro	Arg	Ala	Cys	Gln 70	Ile	Phe	Ile	Cys	His 75	Ile	Cys	Glu	Glu	Asp 80	
acc	cac	ctt	gca	gag	acg	ctg	ggg	ctc	tcc	tca	agc	cca	caa	tct	gga	288
Thr	His	Leu	Ala	Glu 85	Thr	Leu	Gly	Leu	Ser 90	Ser	Ser	Pro	Gln	Ser 95	Gly	
aat	tct	cag	aac	acc	acg	gac	tct	gaa	gta	gcg	ttt	cct	cct	ctt	cca	336
Asn	Ser	Gln	Asn 100	Thr	Thr	Asp	Ser	Glu 105	Val	Ala	Phe	Pro	Pro	Leu 110	Pro	
gcc	agc	gtg	aat	aac	atg	cct	ggg	ccg	gct	gag	cca	gaa	gaa	tct	gta	384
Ala	Ser	Val	Asn 115	Asn	Met	Pro	Gly 120	Pro	Ala	Glu	Pro	Glu 125	Glu	Ser	Val	
gat	gct	ctc	aag	ctt	tgt	cct	cgt	gaa	aac	ttc	gtg	aaa	ctg	tgt	aaa	432
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg 135	Glu	Asn	Phe	Val 140	Lys	Leu	Cys	Lys	
cag	agg	gct	gaa	gag	atc	tac	cca	ata	aag	gag	aga	aag	gat	cgt	act	480
Gln	Arg	Ala	Glu	Glu	Ile 150	Tyr	Pro	Ile	Lys	Glu 155	Arg	Lys	Asp	Arg	Thr 160	
cgt	ctg	gct	ctc	atc	ata	tgc	aat	acg	acg	ttc	gat	cat	ctt	tct	ctc	528
Arg	Leu	Ala	Leu	Ile 165	Ile	Cys	Asn	Thr	Thr 170	Phe	Asp	His	Leu	Ser 175	Leu	
agg	aag	ggg	gct	gac	ctt	gac	gtt	gca	ggg	atg	agg	agg	ctg	ctt	aca	576
Arg	Lys	Gly	Ala 180	Asp	Leu	Asp	Val	Ala 185	Gly	Met	Arg	Arg	Leu 190	Leu	Thr	
gac	ctt	ggc	tac	agt	gtg	cac	ata	aaa	gag	gaa	ctc	act	gct	aag	gac	624
Asp	Leu	Gly 195	Tyr	Ser	Val	His	Ile 200	Lys	Glu	Glu	Leu	Thr 205	Ala	Lys	Asp	
atg	gaa	tca	gag	ctg	agg	gca	ttt	gct	gcc	cgt	cca	gag	cac	aag	tcc	672
Met	Glu	Ser	Glu	Leu	Arg	Ala 215	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser	
tcg	gac	agc	aca	ttc	ctg	gtg	ttc	atg	tct	cat	ggc	atc	ctg	agt	gga	720
Ser	Asp	Ser	Thr	Phe	Leu 230	Val	Phe	Met	Ser	His 235	Gly	Ile	Leu	Ser 240	Gly	
atc	tgt	ggg	acg	aag	tac	agc	gct	gaa	gga	gac	cca	gat	gta	ttg	gct	768
Ile	Cys	Gly	Thr	Lys 245	Tyr	Ser	Ala	Glu	Gly 250	Asp	Pro	Asp	Val	Leu 255	Ala	
tat	gac	acc	atc	ttc	cag	att	ttc	aac	aac	cgc	aac	tgc	ctt	agt	cta	816
Tyr	Asp	Thr	Ile	Phe 260	Gln	Ile	Phe	Asn 265	Asn	Arg	Asn	Cys	Leu	Ser 270	Leu	
aag	gac	aag	ccc	aag	gtc	atc	atc	gtc	cag	gcc	tgc	aga	ggg	gaa	aat	864
Lys	Asp	Lys 275	Pro	Lys	Val	Ile	Ile	Val 280	Gln	Ala	Cys	Arg	Gly	Glu	Asn	
ttg	ggg	gaa	ctg	ttg	atc	agt	gac	tct	cca	gcg	gcc	cca	atg	gac	agc	912
Leu	Gly	Glu	Leu	Leu	Ile	Ser	Asp	Ser	Pro	Ala	Ala	Pro	Met	Asp	Ser	

290	295	300	
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag			960
Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu			
305	310	315	320
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc			1008
Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe			
	325	330	335
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga			1056
Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly			
	340	345	350
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg			1104
Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp			
	355	360	365
tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa			1152
Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu			
	370	375	380
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg			1200
Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met			
385	390	395	400
aca aga tgt ttc tac ctc ttc cca gga cat taa			1233
Thr Arg Cys Phe Tyr Leu Phe Pro Gly His			
	405	410	

<210> 15  
 <211> 410  
 <212> PRT  
 <213> Felis catus

<400> 15

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20 25 30

Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala
35 40 45

Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys
50 55 60

Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp
65 70 75 80

Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly  
 85 90 95

Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro  
 100 105 110

Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val  
 115 120 125

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys  
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr  
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu  
 165 170 175

Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr  
 180 185 190

Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp  
 195 200 205

Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser  
 210 215 220

Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly  
 225 230 235 240

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala  
 245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu  
 260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn  
 275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser  
 290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu  
 305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe  
 325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly  
 340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp  
 355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu  
 370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met  
 385 390 395 400

Thr Arg Cys Phe Tyr Leu Phe Pro Gly His  
 405 410

<210> 16  
 <211> 1233  
 <212> DNA  
 <213> Felis catus

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 atgaaagcac cacgaatact tttggaagca cgtgatgagt tgtgtaatga agagagatcc 180  
 cttgttcacg tctctccaag acacatgatg tggggtcgag gagcagaaag cgatgaagtc 240  
 cttctccacg tggaccttgt aaatggcgtc gtcctctagg ttgtcaccca cctgtgaaag 300  
 gctgctaccc atctgtgaag tgctgtccat tggggccgct ggagagtcac tgatcaacag 360  
 ttcccccaaa ttttcacctc tgcaggcctg gacgatgatg accttgggct tgtcctttag 420  
 actaaggcag ttgcggttgt tgaaaatctg gaagatggtg tcataagcca atacatctgg 480  
 gtctccttca gcgctgtact tcgtcccaca gattccactc aggatgccat gagacatgaa 540  
 caccaggaat gtgctgtccg aggacttggt ctctggacgg gcagcaaatg ccctcagctc 600  
 tgattccatg tccttagcag tgagttcctc ttttatgtgc aactgtagc caaggtctgt 660  
 aagcagcctc ctcacccctg caacgtcaag gtcagccccc ttctgagag aaagatgatc 720

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gaacgtcgta ttgcatatga tgagagccag acgagtacga tcctttctct cctttattgg      780
gtagatctct tcagccctct gtttacacag tttcacgaag ttttcacgag gacaaagctt      840
gagagcatct acagattctt ctggctcagc cggcccaggc atgttattca cgctggctgg      900
aagaggagga aacgctactt cagagtcctg ggtgttctga gaatttccag attgtgggct      960
tgaggagagc cccagcgtct ctgcaagggtg ggtgtcttcc tcacagatgt gacagataaa    1020
gatctggcac gcccggtggcc ctttccgcag gacgctgtcg atcagagctc gggccttgtc    1080
cataacggta gcgtttttcac attttactct ctccatctcc tcctggttca gcacgttttt    1140
ctcaaagagt tcatccagca agccgttgac cgtcccatg ccgactgagt tgatgaactg      1200
cttcctcttc tccttcagga ccttgtcggc cat                                  1233

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<210> 17
<211> 526
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (18)..(524)

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           1             5             10

cag ttc atc aac tca gtc ggc atg ggg acg gtc aac ggc ttg ctg gat      98
Gln Phe Ile Asn Ser Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp
           15             20             25

gaa ctc ttt gag aaa aac gtg ctg aac cag gag gag atg gag aga gta      146
Glu Leu Phe Glu Lys Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val
           30             35             40

aaa tgt gaa aac gct acc gtt atg gac aag gcc cga gct ctg atc gac      194
Lys Cys Glu Asn Ala Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp
           45             50             55

agc gtc ctg cgg aaa ggg cca cgg gcg tgc cag atc ttt atc tgt cac      242
Ser Val Leu Arg Lys Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His
           60             65             70             75

atc tgt gag gaa gac acc cac ctt gca gag acg ctg ggg ctc tcc tca      290
Ile Cys Glu Glu Asp Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser
           80             85             90

agc cca caa tct gga aat tct cag aac acc acg gac tct gaa gta gcg      338
Ser Pro Gln Ser Gly Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala

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	95		100		105	
ttt cct cct ctt cca gcc agc gtg aat aac atg cct ggg ccg gct gag						386
Phe Pro Pro Leu Pro Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu						
	110		115		120	
cca gaa gaa tct gta gat gct ctc aag ctt tgt cct cgt gaa aac ttc						434
Pro Glu Glu Ser Val Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe						
	125		130		135	
gtg aaa ctg tgt aaa cag agg gct gaa gag atc tac cca ata aag gag						482
Val Lys Leu Cys Lys Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu						
	140		145		150	155
aga aag gat cgt act cgt ctg gct ctc atc ata tgc aat acg ac						526
Arg Lys Asp Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Thr						
	160		165			
<210>	18					
<211>	169					
<212>	PRT					
<213>	Felis catus					
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Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys						
	20		25		30	
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala						
	35		40		45	
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys						
	50		55		60	
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp						
65	70		75		80	
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly						
	85		90		95	
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro						
	100		105		110	
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val						
	115		120		125	

Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys  
 130 135 140

Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr  
 145 150 155 160

Arg Leu Ala Leu Ile Ile Cys Asn Thr  
 165

<210> 19  
 <211> 526  
 <212> DNA  
 <213> Felis catus

<400> 19  
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 atctcttcag ccctctgttt acacagtttc acgaagtgtt cagcaggaca aagcttgaga 120  
 gcatctacag attcttctgg ctccagccggc ccaggcatgt tattcacgct ggctggaaga 180  
 ggaggaaacg ctacttcaga gtccgtggtg ttctgagaat ttccagattg tgggcttgag 240  
 gagagcccca gcgtctctgc aagggtgggtg tcttcctcac agatgtgaca gataaagatc 300  
 tggcacgccc gtggcccttt ccgcaggacg ctgtcgatca gagctcgggc cttgtccata 360  
 acggtagcgt tttcacattt tactctctcc atctcctcct gggttcagcac gtttttctca 420  
 aagagttcat ccagcaagcc gttgaccgtc cccatgccga ctgagttgat gaactgcttc 480  
 ctcttgccct tcagatcctt gtcggccatg gctttttgct cgtgcc 526

<210> 20  
 <211> 500  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (3)..(362)

<220>  
 <221> misc\_feature  
 <222> (473)..(473)  
 <223> n = unknown at position 473

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 Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser Thr  
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tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag gac	95
Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp	
20 25 30	
gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc tgc	143
Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys	
35 40 45	
tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga tct	191
Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser	
50 55 60	
ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg tgc	239
Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys	
65 70 75	
ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa aaa	287
Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys	
80 85 90 95	
cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg aca	335
Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr	
100 105 110	
aga tac ttc tat ctc ttc cct ggc aat tgaaaatagc aatcatgggc	382
Arg Tyr Phe Tyr Leu Phe Pro Gly Asn	
115 120	
agtcagccc ttcttgacca acttggaata gtaccttagc tagcacaaca cactcattta	442
acgttttggtat tctcaataaaa aatgaaaaca nctaaaaaaa aaaaaaaaaa aaaaaaaaaa	500

<210> 21  
 <211> 120  
 <212> PRT  
 <213> Felis catus

<400> 21

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Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu Asp Asp	
20 25 30	
Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe Cys Ser	
35 40 45	
Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly Ser Leu	
50 55 60	

Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp Cys Phe  
65 70 75 80

His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu Lys Pro  
85 90 95

Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met Thr Arg  
100 105 110

Tyr Phe Tyr Leu Phe Pro Gly Asn  
115 120

<210> 22  
<211> 500  
<212> DNA  
<213> Felis catus

<220>  
<221> misc\_feature  
<222> (28)..(28)  
<223> n = unknown at position 28

<400> 22  
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ccatgattgc ttttttcaat tgccagggaa gagatagaag tatcttgtca tggatagtcg 180  
ttcaatgggtg ggcatctggg ctctaacttt tggtttttca aatgactgtt gtaccttccg 240  
aaatacttcc tccagatgaa agcaccacga atacttttgg aagcacgtga tgagttgtgt 300  
aatgaagaga gatcccttgt tcacgtctct ccaagacaca tgatgtgggg tcgaggagca 360  
gaaagcgatg aagtccttct ccacgtggac cttgtaaatg gcgtcgtcct ctaggttgtc 420  
accacactgt gaaaggctgc taccatctg tgaagtgtg tccattgggg ccgctggaga 480  
gtcactgatc aacagttccc 500

<210> 23  
<211> 1230  
<212> DNA  
<213> Felis catus

<220>  
<221> CDS  
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1	5 10 15															
gtc ggc atg ggg acg gtc aac ggc ttg ctg gat gaa ctc ttt gag aaa																96
Val Gly Met Gly Thr Val Asn Gly Leu Leu Asp Glu Leu Phe Glu Lys																
	20 25 30															
aac gtg ctg aac cag gag gag atg gag aga gta aaa tgt gaa aac gct																144
Asn Val Leu Asn Gln Glu Glu Met Glu Arg Val Lys Cys Glu Asn Ala																
	35 40 45															
acc gtt atg gac aag gcc cga gct ctg atc gac agc gtc ctg cgg aaa																192
Thr Val Met Asp Lys Ala Arg Ala Leu Ile Asp Ser Val Leu Arg Lys																
	50 55 60															
ggg cca cgg gcg tgc cag atc ttt atc tgt cac atc tgt gag gaa gac																240
Gly Pro Arg Ala Cys Gln Ile Phe Ile Cys His Ile Cys Glu Glu Asp																
65	70 75 80															
acc cac ctt gca gag acg ctg ggg ctc tcc tca agc cca caa tct gga																288
Thr His Leu Ala Glu Thr Leu Gly Leu Ser Ser Ser Pro Gln Ser Gly																
	85 90 95															
aat tct cag aac acc acg gac tct gaa gta gcg ttt cct cct ctt cca																336
Asn Ser Gln Asn Thr Thr Asp Ser Glu Val Ala Phe Pro Pro Leu Pro																
	100 105 110															
gcc agc gtg aat aac atg cct ggg ccg gct gag cca gaa gaa tct gta																384
Ala Ser Val Asn Asn Met Pro Gly Pro Ala Glu Pro Glu Glu Ser Val																
	115 120 125															
gat gct ctc aag ctt tgt cct cgt gaa aac ttc gtg aaa ctg tgt aaa																432
Asp Ala Leu Lys Leu Cys Pro Arg Glu Asn Phe Val Lys Leu Cys Lys																
	130 135 140															
cag agg gct gaa gag atc tac cca ata aag gag aga aag gat cgt act																480
Gln Arg Ala Glu Glu Ile Tyr Pro Ile Lys Glu Arg Lys Asp Arg Thr																
145	150 155 160															
cgt ctg gct ctc atc ata tgc aat acg acg ttc gat cat ctt tct ctc																528
Arg Leu Ala Leu Ile Ile Cys Asn Thr Thr Phe Asp His Leu Ser Leu																
	165 170 175															
agg aag ggg gct gac ctt gac gtt gca ggg atg agg agg ctg ctt aca																576
Arg Lys Gly Ala Asp Leu Asp Val Ala Gly Met Arg Arg Leu Leu Thr																
	180 185 190															
gac ctt ggc tac agt gtg cac ata aaa gag gaa ctc act gct aag gac																624
Asp Leu Gly Tyr Ser Val His Ile Lys Glu Glu Leu Thr Ala Lys Asp																
	195 200 205															
atg gaa tca gag ctg agg gca ttt gct gcc cgt cca gag cac aag tcc																672
Met Glu Ser Glu Leu Arg Ala Phe Ala Ala Arg Pro Glu His Lys Ser																
	210 215 220															

tcg gac agc aca ttc ctg gtg ttc atg tct cat ggc atc ctg agt gga Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Leu Ser Gly 225 230 235 240	720
atc tgt ggg acg aag tac agc gct gaa gga gac cca gat gta ttg gct Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala 245 250 255	768
tat gac acc atc ttc cag att ttc aac aac cgc aac tgc ctt agt cta Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu 260 265 270	816
aag gac aag ccc aag gtc atc atc gtc cag gcc tgc aga ggt gaa aat Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn 275 280 285	864
ttg ggg gaa ctg ttg atc agt gac tct cca gcg gcc cca atg gac agc Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser 290 295 300	912
act tca cag atg ggt agc agc ctt tca cag gtg ggt gac aac cta gag Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu 305 310 315 320	960
gac gac gcc att tac aag gtc cac gtg gag aag gac ttc atc gct ttc Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe 325 330 335	1008
tgc tcc tcg acc cca cat cat gtg tct tgg aga gac gtg aac aag gga Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly 340 345 350	1056
tct ctc ttc att aca caa ctc atc acg tgc ttc caa aag tat tcg tgg Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp 355 360 365	1104
tgc ttt cat ctg gag gaa gta ttt cgg aag gta caa cag tca ttt gaa Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu 370 375 380	1152
aaa cca aat gtt aga gcc cag atg ccc acc att gaa cga cta tcc atg Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met 385 390 395 400	1200
aca aga tac ttc tat ctc ttc cct ggc aat Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn 405 410	1230

<210> 24  
 <211> 410  
 <212> PRT  
 <213> Felis catus

<400> 24

Met Ala Asp Lys Asp Leu Lys Gly Lys Arg Lys Gln Phe Ile Asn Ser

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Val	Gly	Met	Gly	Thr	Val	Asn	Gly	Leu	Leu	Asp	Glu	Leu	Phe	Glu	Lys		
			20					25					30				
Asn	Val	Leu	Asn	Gln	Glu	Glu	Met	Glu	Arg	Val	Lys	Cys	Glu	Asn	Ala		
		35					40					45					
Thr	Val	Met	Asp	Lys	Ala	Arg	Ala	Leu	Ile	Asp	Ser	Val	Leu	Arg	Lys		
	50					55					60						
Gly	Pro	Arg	Ala	Cys	Gln	Ile	Phe	Ile	Cys	His	Ile	Cys	Glu	Glu	Asp		
65					70					75					80		
Thr	His	Leu	Ala	Glu	Thr	Leu	Gly	Leu	Ser	Ser	Ser	Pro	Gln	Ser	Gly		
				85					90					95			
Asn	Ser	Gln	Asn	Thr	Thr	Asp	Ser	Glu	Val	Ala	Phe	Pro	Pro	Leu	Pro		
			100					105					110				
Ala	Ser	Val	Asn	Asn	Met	Pro	Gly	Pro	Ala	Glu	Pro	Glu	Glu	Ser	Val		
		115					120					125					
Asp	Ala	Leu	Lys	Leu	Cys	Pro	Arg	Glu	Asn	Phe	Val	Lys	Leu	Cys	Lys		
	130					135					140						
Gln	Arg	Ala	Glu	Glu	Ile	Tyr	Pro	Ile	Lys	Glu	Arg	Lys	Asp	Arg	Thr		
145					150					155					160		
Arg	Leu	Ala	Leu	Ile	Ile	Cys	Asn	Thr	Thr	Phe	Asp	His	Leu	Ser	Leu		
				165					170					175			
Arg	Lys	Gly	Ala	Asp	Leu	Asp	Val	Ala	Gly	Met	Arg	Arg	Leu	Leu	Thr		
			180					185					190				
Asp	Leu	Gly	Tyr	Ser	Val	His	Ile	Lys	Glu	Glu	Leu	Thr	Ala	Lys	Asp		
		195					200					205					
Met	Glu	Ser	Glu	Leu	Arg	Ala	Phe	Ala	Ala	Arg	Pro	Glu	His	Lys	Ser		
	210					215					220						
Ser	Asp	Ser	Thr	Phe	Leu	Val	Phe	Met	Ser	His	Gly	Ile	Leu	Ser	Gly		
225					230					235					240		

Ile Cys Gly Thr Lys Tyr Ser Ala Glu Gly Asp Pro Asp Val Leu Ala  
 245 250 255

Tyr Asp Thr Ile Phe Gln Ile Phe Asn Asn Arg Asn Cys Leu Ser Leu  
 260 265 270

Lys Asp Lys Pro Lys Val Ile Ile Val Gln Ala Cys Arg Gly Glu Asn  
 275 280 285

Leu Gly Glu Leu Leu Ile Ser Asp Ser Pro Ala Ala Pro Met Asp Ser  
 290 295 300

Thr Ser Gln Met Gly Ser Ser Leu Ser Gln Val Gly Asp Asn Leu Glu  
 305 310 315 320

Asp Asp Ala Ile Tyr Lys Val His Val Glu Lys Asp Phe Ile Ala Phe  
 325 330 335

Cys Ser Ser Thr Pro His His Val Ser Trp Arg Asp Val Asn Lys Gly  
 340 345 350

Ser Leu Phe Ile Thr Gln Leu Ile Thr Cys Phe Gln Lys Tyr Ser Trp  
 355 360 365

Cys Phe His Leu Glu Glu Val Phe Arg Lys Val Gln Gln Ser Phe Glu  
 370 375 380

Lys Pro Asn Val Arg Ala Gln Met Pro Thr Ile Glu Arg Leu Ser Met  
 385 390 395 400

Thr Arg Tyr Phe Tyr Leu Phe Pro Gly Asn  
 405 410

<210> 25  
 <211> 1230  
 <212> DNA  
 <213> Felis catus

<400> 25  
 attgccaggg aagagataga agtatcttgt catggatagt cgttcaatgg tgggcatctg 60  
 ggctctaaca tttggttttt caaatgactg ttgtaccttc cgaaatactt cctccagatg 120  
 aaagcaccac gaatactttt ggaagcacgt gatgagttgt gtaatgaaga gagatccctt 180



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gttcacgtct ctccaagaca catgatgtgg ggctcaggag cagaaagcga tgaagtcctt 240
ctccacgtgg accttgtaaa tggcgtcgtc ctctaggttg tcacccacct gtgaaaggct 300
gctacccatc tgtgaagtgc tgtccattgg ggccgctgga gagtcactga tcaacagttc 360
ccccaaattt tcacctctgc aggccctggac gatgatgacc ttgggcttgt cctttagact 420
aaggcagttg cggttgttga aaatctggaa gatggtgtca taagccaata catctgggtc 480
tccttcagcg ctgtacttcg tcccacagat tccactcagg atgccatgag acatgaacac 540
caggaatgtg ctgtccgagg acttgtgctc tggacgggca gcaaagccc tcagctctga 600
ttccatgtcc ttagcagtga gttcctcttt tatgtgcaca ctgtagccaa ggtctgtaag 660
cagcctcctc atccctgcaa cgtcaaggtc agcccccttc ctgagagaaa gatgatcgaa 720
cgtcgtattg catatgatga gagccagacg agtacgatcc tttctctcct ttattgggta 780
gatctcttca gccctctgtt tacacagttt cacgaagttt tcacgaggac aaagcttgag 840
agcatctaca gattcttctg gctcagccgg cccaggcatg ttattcacgc tggctggaag 900
aggaggaaac gctacttcag agtcctgtgg gttctgagaa tttccagatt gtgggcttga 960
ggagagcccc agcgtctctg caagggtgggt gtcttcctca cagatgtgac agataaagat 1020
ctggcacgcc cgtggccctt tccgcaggac gctgtcgatc agagctcggg ccttgtccat 1080
aacggtagcg ttttcacatt ttactctctc catctcctcc tggttcagca cgtttttctc 1140
aaagagttca tccagcaagc cgttgaccgt ccccatgccg actgagttga tgaactgctt 1200
cctcttgccc ttcagatcct tgtcggccat 1230

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<210> 26
<211> 921
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(921)

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<400> 26
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Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa 96
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu
20 25 30

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gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly 35 40 45	144
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly 50 55 60	192
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu 65 70 75 80	240
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg 85 90 95	288
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys 100 105 110	336
aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr 115 120 125	384
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln 130 135 140	432
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val 145 150 155 160	480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser 165 170 175	528
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp 180 185 190	576
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile 195 200 205	624
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro 210 215 220	672
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr 225 230 235 240	720
tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255	768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag	816

Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Ser	Val	Asp	Lys		
			260					265					270				
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa		864
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln		
		275					280					285					
gcc	aga	gac	cgc	tac	tat	agc	tca	tcc	tgg	agc	aac	tgg	gca	tcc	gtg		912
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asn	Trp	Ala	Ser	Val		
	290					295					300						
tcc	tgc	agt															921
Ser	Cys	Ser															
305																	
<210> 27																	
<211> 307																	
<212> PRT																	
<213> Felis catus																	
<400> 27																	
Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His		
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Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	Asn	Thr	Pro	Glu		
		20					25					30					
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln	Ser	Ser	Glu	Val	Leu	Gly		
	35						40					45					
Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	Glu	Phe	Ala	Asp	Ala	Gly		
	50					55					60						
Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Glu	Val	Leu	Ser	His	Ser	Phe	Leu		
65				70				75							80		
Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	Ser	Thr	Asp	Ile	Leu	Arg		
			85					90						95			
Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys		
		100						105					110				
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr		
		115					120					125					
Asp	Leu	Lys	Phe	Thr	Val	Lys	Ser	Ser	Arg	Gly	Ser	Ser	Asp	Pro	Gln		
	130					135					140						

Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val  
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
 165 170 175

Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro  
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val  
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys  
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val  
 290 295 300

Ser Cys Ser  
 305

<210> 28  
 <211> 921  
 <212> DNA  
 <213> Felis catus

<400> 28  
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 cacgcggatc ttggcattct tgtggcacac gaccttggct gaggtcttgt ccacggagag 120  
 tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaatg ttaaggagaa 180

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gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctacttcca catgccgaga 240
attttttaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat 300
gaagaagctg ctggtgtagt tttcgtactt gagcttgtga atagcgtcca ccacgacttc 360
aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta 420
cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca 480
agtcacctct tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatcggg 540
actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt 600
tagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660
atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca 720
gggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc 780
taggacttca ctgctctggg cagagggtcca ggtgatgtca tcttcttcag gagtattgca 840
ggtgaggacc accatttctc cgggggcacg aggggtgccag tccaactcta caacataaac 900
gtttttctcc agttcccata t 921

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<210> 29
<211> 987
<212> DNA
<213> Felis catus

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<220>
<221> CDS
<222> (1)..(987)

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<400> 29
atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg 48
Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1 5 10 15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys

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65	70	75	80	
gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt				288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val	85	90	95	
ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg				336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	100	105	110	
tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt				384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	115	120	125	
cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg				432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	130	135	140	
ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga				480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg	145	150	155	160
ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca				528
Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser	165	170	175	
gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg				576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	180	185	190	
gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc				624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro	195	200	205	
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac				672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	210	215	220	
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag				720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys	225	230	235	240
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc				768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	245	250	255	
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta				816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	260	265	270	
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac				864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	275	280	285	
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat				912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	290	295	300	

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg 960  
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

agc aac tgg gca tcc gtg tcc tgc agt 987  
 Ser Asn Trp Ala Ser Val Ser Cys Ser  
 325

<210> 30  
 <211> 329  
 <212> PRT  
 <213> Felis catus

<400> 30

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
 85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
 145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
 165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
 180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
 195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
 210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
 225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
 245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
 260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
 275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser  
 325

<210> 31  
 <211> 987  
 <212> DNA  
 <213> Felis catus

<400> 31  
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 cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtccttg ccacggagag 120  
 tctgtctttc ttttctctgt tgttcttgcc ctggacctgt acgccaaatg ttaaggagaa 180  
 gtaggaatgt ggggtgctcc aggtgtcagg gtattcccag ctcacttcca catgccgaga 240



attttttaat ggcttcagtt gcaggttctt ggggtgggtcc ggtttgatga tgtccctgat	300
gaagaagctg ctgggtgtagt tttcgtactt gagcttgatga atagcgtcca ccacgacttc	360
aatgggtagg ctctcctcgg cagccgggca ggcactgccc tcctgacact ccactgtgta	420
cttcttataa tccctgttgt ccactctgac cttctctgct gagagtgtcg ctgctccaca	480
agtcaccctt tgggggtcag aggagcctct gctgcttttg acagtgaatt tcaaatcggt	540
actgattgcc gtcagccacc agcaggtgaa acgtccagaa taattctttg cctcacattt	600
tagaaagatc ttatttttgg attctttctg ttcccttaag atatcagtgg accaaattcc	660
atcttccttt ttgtgtatca ggaggaacga atggctcaga acctcgctc ctttatgaca	720
ggtatactgg ccagcatctg caaattcttt gacttggatg gtcagagttt taccagagcc	780
taggacttca ctgctctggg cagaggtcca ggtgatgtca tcttcttcag gagtattgca	840
ggtgaggacc accatttctc cgggggcac aggggtgccag tccaactcta caacataaac	900
gtttttctcc agttcccata tggccatgag gggaggtgcc agcaaaacca gggaaaacca	960
ggcgatgacc aactgctgag gatgcat	987

<210> 32  
 <211> 666  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(666)

<400> 32 atg tgc ccg ccg cgt ggc ctc ctc ctt gta acc atc ctg gtc ctg tta Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu 1 5 10 15	48
aac cac ctg gac cac ctc agt ttg gcc agg aac ctc ccc aca ccc aca Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr 20 25 30	96
cca agc cca gga atg ttc cag tgc ctc aac cac tcc caa acc ctg ctg Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu 35 40 45	144
cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa ttt Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe 50 55 60	192
tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa gat Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	240

65	70	75	80	
aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat				288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn	85	90	95	
gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg agt				336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser	100	105	110	
tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc				384
Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser	115	120	125	
agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg				432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met	130	135	140	
aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa				480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln	145	150	155	160
aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc aac				528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn	165	170	175	
agt gtg act gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat				576
Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr	180	185	190	
aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt				624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg	195	200	205	
gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc				666
Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser	210	215	220	

<210> 33  
 <211> 222  
 <212> PRT  
 <213> Felis catus

<400> 33

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

Asn His Leu Asp His Leu Ser Leu Ala Arg Asn Leu Pro Thr Pro Thr
20 25 30

Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu
35 40 45

Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe  
 50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
 65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
 85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
 100 105 110

Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser  
 115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met  
 130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
 145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn  
 165 170 175

Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
 180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg  
 195 200 205

Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
 210 215 220

<210> 34  
 <211> 666  
 <212> DNA  
 <213> Felis catus

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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120  
 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180

catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc	240
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt	300
cataaaagag gtctttcttg aggccaggca actcccatta gttatcagag agatctctct	360
ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct	420
ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc	480
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg	540
gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggagggttc tggccaaact	600
gaggtggtcc aggtggttta acaggaccag gatgggtaca aggaggaggc cacgcggcgg	660
gcacat	666

<210> 35  
 <211> 591  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(591)

<400> 35																
agg aac ctc ccc aca ccc aca cca agc cca gga atg ttc cag tgc ctc	48															
Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu																
1 5 10 15																
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag																96
Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys																
20 25 30																
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat																144
Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp																
35 40 45																
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta																192
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu																
50 55 60																
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc																240
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile																
65 70 75 80																
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt																288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe																
85 90 95																
atg acg acc ctg tgc ctt agc agt atc tat gag gac ttg aag atg tac																336
Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr																
100 105 110																

cag	gtg	gag	ttc	aag	gcc	atg	aat	gca	aag	ctg	tta	atg	gat	cct	aaa	384
Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	
	115						120						125			

agg	cag	atc	ttt	ctg	gat	caa	aac	atg	ctg	aca	gct	att	gat	gag	ctg	432
Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	
	130					135					140					

tta	cag	gcc	ctg	aat	gtc	aac	agt	gtg	act	gtg	cca	cag	aac	tcc	tcc	480
Leu	Gln	Ala	Leu	Asn	Val	Asn	Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser	
	145				150					155					160	

ttg	gaa	gaa	ccg	gat	ttt	tat	aaa	act	aaa	atc	aag	ctc	tgc	ata	ctt	528
Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	
				165					170					175		

ctt	cat	gct	ttc	aga	att	cgt	gca	gtg	acc	atc	aat	aga	atg	atg	agc	576
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser	
			180					185					190			

tat	ctg	aat	gct	tcc												591
Tyr	Leu	Asn	Ala	Ser												
			195													

<210> 36  
 <211> 197  
 <212> PRT  
 <213> Felis catus

<400> 36

Arg	Asn	Leu	Pro	Thr	Pro	Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu
1				5					10					15	

Asn	His	Ser	Gln	Thr	Leu	Leu	Arg	Ala	Ile	Ser	Asn	Thr	Leu	Gln	Lys
			20					25					30		

Ala	Arg	Gln	Thr	Leu	Glu	Phe	Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp
		35					40					45			

His	Glu	Asp	Ile	Thr	Lys	Asp	Lys	Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu
	50					55					60				

Pro	Leu	Glu	Leu	Thr	Met	Asn	Glu	Ser	Cys	Leu	Ala	Ser	Arg	Glu	Ile
65					70					75					80

Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe
				85					90					95	

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
100 105 110

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
115 120 125

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
130 135 140

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser  
145 150 155 160

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
165 170 175

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
180 185 190

Tyr Leu Asn Ala Ser  
195

<210> 37  
<211> 591  
<212> DNA  
<213> Felis catus

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aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120  
ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180  
catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300  
cataaaagag gtctttctgg aggccaggca actcccatta gttatcagag agatctctct 360  
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccactgtgct 420  
ggttttatct tttgtgatat cttcatgac aatctcttcg gaagtgcagg agtaaaattc 480  
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540  
gttgaggcac tggaacattc ctgggcttgg tgtgggtgtg gggaggttcc t 591

<210> 38  
<211> 1599

<212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
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<400> 38
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Met His Pro Gln Gln Leu Val Ile Ala Trp Leu Ser Leu Val Leu Leu
1          5          10          15

gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt      96
Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
          20          25          30

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc     144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
          35          40          45

acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag     192
Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
          50          55          60

agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa     240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
65          70          75          80

gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt     288
Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
          85          90          95

ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg     336
Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp
          100          105          110

tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt     384
Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe
          115          120          125

cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg     432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
          130          135          140

ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga     480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg
145          150          155          160

ggc tcc tct gac ccc caa gag gtg act tgt gga gca gcg aca ctc tca     528
Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser
          165          170          175

gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg     576
Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val
          180          185          190

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gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro 195 200 205	624
att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys 225 230 235 240	720
aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc aac tgg gca tcc gtg tcc tgc agt ggt ggc ggt ggc ggc gga tct Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggg atg ttc cag tgc ctc Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ctg ctg cga gcc atc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa ttt tac tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp 370 375 380	1152
cat gaa gat atc aca aaa gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu 385 390 395 400	1200
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile 405 410 415	1248
tct ctg ata act aat ggg agt tgc ctg gcc tcc aga aag acc tct ttt	1296



Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Arg	Lys	Thr	Ser	Phe	
			420					425					430			
atg	acg	acc	ctg	tgc	ctt	agc	agt	atc	tat	gag	gac	ttg	aag	atg	tac	1344
Met	Thr	Thr	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr	
		435					440					445				
cag	gtg	gag	ttc	aag	gcc	atg	aat	gca	aag	ctg	tta	atg	gat	cct	aaa	1392
Gln	Val	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys	
	450					455					460					
agg	cag	atc	ttt	ctg	gat	caa	aac	atg	ctg	aca	gct	att	gat	gag	ctg	1440
Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu	
465				470					475						480	
tta	cag	gcc	ctg	aat	gtc	aac	agt	gtg	act	gtg	cca	cag	aac	tcc	tcc	1488
Leu	Gln	Ala	Leu	Asn	Val	Asn	Ser	Val	Thr	Val	Pro	Gln	Asn	Ser	Ser	
			485					490					495			
ttg	gaa	gaa	ccg	gat	ttt	tat	aaa	act	aaa	atc	aag	ctc	tgc	ata	ctt	1536
Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu	
			500				505					510				
ctt	cat	gct	ttc	aga	att	cgt	gca	gtg	acc	atc	aat	aga	atg	atg	agc	1584
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asn	Arg	Met	Met	Ser	
		515				520					525					
tat	ctg	aat	gct	tcc												1599
Tyr	Leu	Asn	Ala	Ser												
	530															

<210> 39  
 <211> 533  
 <212> PRT  
 <213> Felis catus

<400> 39

Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ala	Trp	Leu	Ser	Leu	Val	Leu	Leu
1			5					10					15		
Ala	Pro	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asn	Val	Tyr	Val
			20					25				30			
Val	Glu	Leu	Asp	Trp	His	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu
	35					40					45				
Thr	Cys	Asn	Thr	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Asp	Gln
	50				55					60					
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys
65					70				75						80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
145 150 155 160

Gly Ser Ser Asp Pro Gln Glu Val Thr Cys Gly Ala Ala Thr Leu Ser  
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Ser  
 325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu  
 340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys  
 355 360 365

Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
 370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
 385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
 405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe  
 420 425 430

Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
 435 440 445

Gln Val Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
 450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
 465 470 475 480

Leu Gln Ala Leu Asn Val Asn Ser Val Thr Val Pro Gln Asn Ser Ser  
 485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
 500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
 515 520 525

Tyr Leu Asn Ala Ser  
530

<210> 40  
<211> 1599  
<212> DNA  
<213> Felis catus

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ctgtggcaca gtcacactgt tgacattcag ggccgtgaac agctcatcaa tagctgtcag 180  
catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcgt 300  
cataaaagag gtcttttctgg aggccaggca actcccatta gttatcagag agatctctct 360  
ggaagccagg caactctcat tcatggttaa ttccagtggg aagcaggcct ccactgtgct 420  
ggtttttatct tttgtgatat cttcatgatc aatctcttcg gaagtgcagg agtaaaattc 480  
tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540  
gttgaggcac tggaacatcc ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600  
gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660  
gtctctggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggctctt 720  
gtccacggag agtctgtctt tcttttctct gttgttcttg ccctggacct gtacgcaaaa 780  
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cacatgccga gaatttttta atggcttcag ttgcagggtc ttgggtgggt ccggtttgat 900  
gatgtccctg atgaagaagc tgctggtgta gttttcgtac ttgagcttgt gaatagcgtc 960  
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ctccactgtg tacttcttat aatccctggt gtccactctg accttctctg ctgagagtgt 1080  
cgctgtcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtga 1140  
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tgccctacat tttagaaaga tcttattttt ggattcttct tgttccctta agatatcagt 1260  
ggaccaaatt ccatcttcct ttttgtgtat caggaggaac gaatggctca gaacctcgcc 1320  
tcctttatga caggatatac ggccagcatc tgcaaattct ttgacttgga tggtcagagt 1380  
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aggagtattg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500  
 tacaacataa acgtttttct ccagttccca tatggccatg aggggaggtg ccagcaaaac 1560  
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<210> 41  
 <211> 576  
 <212> DNA  
 <213> Felis catus

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 aagactcaaa ttgtatctta tcatcatgtc ctggaacact tctctgaaag aatatgatgt 180  
 catttccttc atcattgata ctctcaggag gactcatttc cttaaaggaa ataattttgt 240  
 tctcacagga gagagtagac atgggtcttat aattcacaga gatggttact gccagacctc 300  
 tagtgaggct atctttatac atatatatga taaattcagt ccgggggtgca ttatctgtac 360  
 agtcagaatc aggcataatc tcaaacacag gttgatctcc ctgggttaatg aagagaactt 420  
 ggtcgttcaa gtttcgtaag attgagagtt tatgttcaag cttgccaaag taatctgttt 480  
 ccagggttttc atcactgtca gctacaaagt aaagtgtatt gtcaataaat ttcattccca 540  
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<400> 42  
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<210> 43  
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cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc aat act cct gaa Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu 20 25 30	96
gaa gat gac atc acc tgg acc tct gac cag agc agt gaa gtc cta ggc Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly 35 40 45	144
tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gca gat gct ggc Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly 50 55 60	192
cag tat acc tgt cat aaa gga ggc gag gtt ctg agc cat tcg ttc ctc Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu 65 70 75 80	240
ctg ata cac aaa aag gaa gat gga att tgg tcc act gat atc tta agg Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg 85 90 95	288
gaa cag aaa gaa tcc aaa aat aag atc ttt cta aaa tgt gag gca aag Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys 100 105 110	336
aat tat tct gga cgt ttc acc tgc tgg tgg ctg acg gca atc agt acc Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr 115 120 125	384
gat ttg aaa ttc act gtc aaa agc agc aga ggc tcc tct gac ccc caa Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln 130 135 140	432
gag gtg act tgt gga gca gcg aca ctc tca gca gag aag gtc aga gtg Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val 145 150 155 160	480
gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser 165 170 175	528
gcc tgc ccg gct gcc gag gag agc cta ccc att gaa gtc gtg gtg gac Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp 180 185 190	576
gct att cac aag ctc aag tac gaa aac tac acc agc agc ttc ttc atc Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile 195 200 205	624
agg gac atc atc aaa ccg gac cca ccc aag aac ctg caa ctg aag cca Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn Leu Gln Leu Lys Pro 210 215 220	672
tta aaa aat tct cgg cat gtg gaa gtg agc tgg gaa tac cct gac acc Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr 225 230 235 240	720

tgg agc acc cca cat tcc tac ttc tcc tta aca ttt ggc gta cag gtc Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Gly Val Gln Val 245 250 255	768
cag ggc aag aac aac aga gaa aag aaa gac aga ctc tcc gtg gac aag Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Ser Val Asp Lys 260 265 270	816
acc tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln 275 280 285	864
gcc aga gac cgc tac tat agc tca tcc tgg agc aac tgg gca tcc gtg Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asn Trp Ala Ser Val 290 295 300	912
tcc tgc agt ggt ggc ggt ggc ggc gga tct aga aac ttg cca acc cct Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro 305 310 315 320	960
act cca tcc ccg ggg atg ttc cag tgc ctc aac cac tcc caa acc ctg Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu 325 330 335	1008
ctg cga gcc atc agc aac acg ctt cag aag gcc aga caa act cta gaa Leu Arg Ala Ile Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu 340 345 350	1056
ttt tac tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aaa Phe Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys 355 360 365	1104
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met 370 375 380	1152
aat gag agt tgc ctg gct tcc aga gag atc tct ctg ata act aat ggg Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly 385 390 395 400	1200
agt tgc ctg gcc tcc aga aag acc tct ttt atg acg acc ctg tgc ctt Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu 405 410 415	1248
agc agt atc tat gag gac ttg aag atg tac cag gtg gag ttc aag gcc Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala 420 425 430	1296
atg aat gca aag ctg tta atg gat cct aaa agg cag atc ttt ctg gat Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp 435 440 445	1344
caa aac atg ctg aca gct att gat gag ctg tta cag gcc ctg aat gtc Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val 450 455 460	1392
aac agt gtg act gtg cca cag aac tcc tcc ttg gaa gaa ccg gat ttt	1440

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe  
 465 470 475 480  
 tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att 1488  
 Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile  
 485 490 495  
 cgt gca gtg acc atc aat aga atg atg agc tat ctg aat gct tcc 1533  
 Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
 500 505 510  
  
 <210> 44  
 <211> 511  
 <212> PRT  
 <213> Felis catus  
  
 <400> 44  
  
 Ile Trp Glu Leu Glu Lys Asn Val Tyr Val Val Glu Leu Asp Trp His  
 1 5 10 15  
  
 Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys Asn Thr Pro Glu  
 20 25 30  
  
 Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln Ser Ser Glu Val Leu Gly  
 35 40 45  
  
 Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Ala Asp Ala Gly  
 50 55 60  
  
 Gln Tyr Thr Cys His Lys Gly Gly Glu Val Leu Ser His Ser Phe Leu  
 65 70 75 80  
  
 Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Arg  
 85 90 95  
  
 Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys  
 100 105 110  
  
 Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr  
 115 120 125  
  
 Asp Leu Lys Phe Thr Val Lys Ser Ser Arg Gly Ser Ser Asp Pro Gln  
 130 135 140  
  
 Glu Val Thr Cys Gly Ala Ala Thr Leu Ser Ala Glu Lys Val Arg Val  
 145 150 155 160



Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser	
				165					170					175		
Ala	Cys	Pro	Ala	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp	
			180					185					190			
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile	
		195					200					205				
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Lys	Asn	Leu	Gln	Leu	Lys	Pro	
	210					215					220					
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr	
225					230					235					240	
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Gly	Val	Gln	Val	
				245					250					255		
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Ser	Val	Asp	Lys	
			260					265					270			
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln	
		275					280					285				
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asn	Trp	Ala	Ser	Val	
	290					295					300					
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Arg	Asn	Leu	Pro	Thr	Pro	
305					310					315					320	
Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu	
				325					330					335		
Leu	Arg	Ala	Ile	Ser	Asn	Thr	Leu	Gln	Lys	Ala	Arg	Gln	Thr	Leu	Glu	
			340					345					350			
Phe	Tyr	Ser	Cys	Thr	Ser	Glu	Glu	Ile	Asp	His	Glu	Asp	Ile	Thr	Lys	
		355					360					365				
Asp	Lys	Thr	Ser	Thr	Val	Glu	Ala	Cys	Leu	Pro	Leu	Glu	Leu	Thr	Met	
	370					375					380					

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly  
 385 390 395 400

Ser Cys Leu Ala Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu  
 405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala  
 420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp  
 435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val  
 450 455 460

Asn Ser Val Thr Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe  
 465 470 475 480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile  
 485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
 500 505 510

<210> 45  
 <211> 1533  
 <212> DNA  
 <213> Felis catus

<400> 45  
 ggaagcattc agatagctca tcattctatt gatggtcact gcacgaattc tgaaagcatg 60  
 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca aggaggagtt 120  
 ctgtggcaca gtcacactgt tgacattcag ggcctgtaac agctcatcaa tagctgtcag 180  
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggctcgt 300  
 cataaaagag gtcttttctgg aggccaggca actcccatta gttatcagag agatctctct 360  
 ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct cactgtgct 420  
 gggttttatct tttgtgatat cttcatgata aatctcttcg gaagtgcagg agtaaaattc 480  
 tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540

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gttgaggcac tggaacatcc ccgggggatgg agtaggggtt ggcaagtttc tagatccgcc 600
gccaccgcca ccactgcagg acacggatgc ccagttgctc caggatgagc tatagtagcg 660
gtctctggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720
gtccacggag agtctgtctt tcttttctct gttgttcttg ccctggacct gtacgccaaa 780
tgttaaggag aagtaggaat gtgggggtgct ccaggtgtca gggattccc agctcacttc 840
cacatgccga gaatttttta atggcttcag ttgcaggttc ttgggtgggt ccggtttgat 900
gatgtccctg atgaagaagc tgctgggtga gttttcgtac ttgagcttgt gaatagcgtc 960
caccacgact tcaatgggta ggctctctc gccagccggg caggcactgc cctcctgaca 1020
ctccactgtg tacttcttat aatccctgtt gtccactctg accttctctg ctgagagtgt 1080
cgctgctcca caagtcacct cttgggggtc agaggagcct ctgctgcttt tgacagtga 1140
tttcaaatcg gtactgattg ccgtcagcca ccagcagggtg aaacgtccag aataattctt 1200
tgctcacat tttagaaaga tcttattttt ggattcttct tgttccctta agatatcagt 1260
ggaccaaatt ccatcttcct ttttgtgtat caggaggaac gaatggctca gaacctcgcc 1320
tcctttatga caggatatac ggccagcatc tgcaaattct ttgacttgga tggtcagagt 1380
tttaccagag cctaggactt cactgctctg gtcagagggtc cagggtgatgt catcttcttc 1440
aggagtattg cagggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500
tacaacataa acgtttttct ccagttccca tat 1533

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<210> 46
<211> 666
<212> DNA
<213> Canis familiaris

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<220>
<221> CDS
<222> (1)..(666)

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<400> 46
atg tgc ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta 48
Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

agc cac ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca 96
Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser
20 25 30

ccg agc cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg 144
Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu
35 40 45

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aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta	192
Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu	
50 55 60	

tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat	240
Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp	
65 70 75 80	

aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat	288
Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn	
85 90 95	

gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt	336
Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser	
100 105 110	

tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc	384
Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser	
115 120 125	

agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg	432
Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met	
130 135 140	

aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa	480
Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln	
145 150 155 160	

aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac	528
Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn	
165 170 175	

agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat	576
Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr	
180 185 190	

aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt	624
Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg	
195 200 205	

gcg gtg acc atc gat aga atg atg agt tat ctg aat tct tcc	666
Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser	
210 215 220	

<210> 47  
 <211> 222  
 <212> PRT  
 <213> Canis familiaris

<400> 47

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu
1 5 10 15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser  
20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu  
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu  
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser  
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met  
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn  
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg  
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser  
210 215 220

<210> 48  
<211> 666  
<212> DNA  
<213> Canis familiaris

<400> 48  
ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg 60  
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120  
ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180  
catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240  
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300  
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360  
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct ccactgtgct 420  
ggtttttatcc tttgtgatat cttcatgac aatctcttcg gaagtgcagg aatataattc 480  
tagagtttgt ctggccttct gaagcgtggt gctgacggct ctgagcaggt tttgggagtg 540  
gttgaggcac tggaatattc ctgggctcgg tgaggctgtg gggaggctcc tggcccaagt 600  
aaggtggtcc aggtggctta gcaggaccag gatggtcaca aggaggaggc cgcgcggcgg 660  
gcacat 666

<210> 49  
<211> 591  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (1)..(591)

<400> 49  
agg agc ctc ccc aca gcc tca ccg agc cca gga ata ttc cag tgc ctc 48  
Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu  
1 5 10 15  
aac cac tcc caa aac ctg ctg aga gcc gtc agc aac acg ctt cag aag 96  
Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys  
20 25 30  
gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat 144  
Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
35 40 45  
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta 192  
His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
50 55 60  
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc 240  
Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
65 70 75 80

tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt	288
Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe	
85 90 95	
atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac	336
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr	
100 105 110	
cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag	384
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys	
115 120 125	
agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg	432
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu	
130 135 140	
tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc	480
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser	
145 150 155 160	
ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt	528
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu	
165 170 175	
ctt cat gct ttc aga att cgt gcg gtg acc atc gat aga atg atg agt	576
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asp Arg Met Met Ser	
180 185 190	
tat ctg aat tct tcc	591
Tyr Leu Asn Ser Ser	
195	

<210> 50  
 <211> 197  
 <212> PRT  
 <213> Canis familiaris

<400> 50

Arg Ser Leu Pro Thr Ala Ser Pro Ser Pro Gly Ile Phe Gln Cys Leu
1 5 10 15

Asn His Ser Gln Asn Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys
20 25 30

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp
35 40 45

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu
50 55 60

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile
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65		70		75		80									
Ser	Leu	Ile	Thr	Asn	Gly	Ser	Cys	Leu	Ala	Ser	Gly	Lys	Ala	Ser	Phe
				85					90					95	
Met	Thr	Val	Leu	Cys	Leu	Ser	Ser	Ile	Tyr	Glu	Asp	Leu	Lys	Met	Tyr
			100					105					110		
Gln	Met	Glu	Phe	Lys	Ala	Met	Asn	Ala	Lys	Leu	Leu	Met	Asp	Pro	Lys
		115					120					125			
Arg	Gln	Ile	Phe	Leu	Asp	Gln	Asn	Met	Leu	Thr	Ala	Ile	Asp	Glu	Leu
	130					135					140				
Leu	Gln	Ala	Leu	Asn	Phe	Asn	Ser	Val	Thr	Val	Pro	Gln	Lys	Ser	Ser
145					150					155					160
Leu	Glu	Glu	Pro	Asp	Phe	Tyr	Lys	Thr	Lys	Ile	Lys	Leu	Cys	Ile	Leu
				165					170					175	
Leu	His	Ala	Phe	Arg	Ile	Arg	Ala	Val	Thr	Ile	Asp	Arg	Met	Met	Ser
		180						185					190		
Tyr	Leu	Asn	Ser	Ser											
		195													

<210> 51  
 <211> 591  
 <212> DNA  
 <213> Canis familiaris

<400> 51	
ggaagaattc agataactca tcattctatc gatggtcacc gcacgaattc tgaaagcatg	60
aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt	120
ctgtggcaca gtcacactgt tgaaattcag ggccctgtaac agctcatcga tagctgtcag	180
catgtttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc	240
cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt	300
cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct	360
ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct cactgtgct	420
ggtttttatcc tttgtgatat cttcatgatc aatctcttcg gaagtgcagg aatataattc	480



tagagtttgt ctggccttct gaagcgtgtt gctgacggct ctcagcaggt tttgggagtg 540

gttgaggcac tggaatatc ctgggctcgg tgaggctgtg gggaggctcc t 591

<210> 52

<211> 921

<212> DNA

<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(921)

<400> 52

ata tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac 48  
Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His  
1 5 10 15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa 96  
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu  
20 25 30

gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt 144  
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly  
35 40 45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc 192  
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly  
50 55 60

cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg 240  
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu  
65 70 75 80

ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag 288  
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys  
85 90 95

gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag 336  
Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys  
100 105 110

aat tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act 384  
Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr  
115 120 125

gat ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa 432  
Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln  
130 135 140

ggg gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg 480  
Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val  
145 150 155 160

gac aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt 528

Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser		
				165					170					175			
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576	
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp		
			180					185					190				
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624	
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile		
		195					200					205					
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672	
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro		
	210					215					220						
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720	
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr		
225				230					235						240		
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768	
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala		
				245					250					255			
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816	
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys		
			260					265					270				
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864	
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln		
		275					280					285					
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912	
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val		
	290					295					300						
tcc	tgc	agt														921	
Ser	Cys	Ser															
305																	

<210> 53  
 <211> 307  
 <212> PRT  
 <213> Canis familiaris

<400> 53

Ile	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val	Val	Glu	Leu	Asp	Trp	His		
1				5					10					15			
Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	Thr	Cys	His	Thr	Pro	Glu		
			20					25					30				
Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Ala	Gln	Ser	Ser	Glu	Val	Leu	Gly		
		35					40					45					

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly  
 50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu  
 65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys  
 85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys  
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr  
 115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln  
 130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val  
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
 165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro  
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala  
 245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys  
 260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
 275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val  
 290 295 300

Ser Cys Ser  
 305

<210> 54  
 <211> 921  
 <212> DNA  
 <213> Canis familiaris

<400> 54  
 actgcaggac acagatgccc agtcgctcca ggatgaacta tagtagcggc ctcgggcttg 60  
 cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtcttgt ccacgcagag 120  
 tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaatg tcaggagaga 180  
 gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga 240  
 atttttcaat ggcttcagct gcaggtttgt ggggtgggtct ggtttgatga tgtctctgat 300  
 gaagaagctg ctgggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc 360  
 gatgggtagg ctctcctcgg cagaggggca ggcactgccc tctgacact ccactgtgta 420  
 cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca 480  
 tgtcaccctt tgggggtcag agaagcctct gctacttttg aactgaatt tcaaatcagt 540  
 actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt 600  
 cagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc 660  
 atcttctttt ttgtgaatca acaggagtga gcggtcaga accttgctc ctttatggca 720  
 ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc 780  
 taggacttca ctgctctgcg ctgagggtcca agtgatgtca tcttcttcag gggtatggca 840  
 ggtgaggacc accatttctc cgggggcacg aggggtgccag tccaactcta caacataaac 900  
 atctttctcc agttcccata t 921

<210> 55  
 <211> 985  
 <212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(984)

<400> 55  
 atg cat cct cag cag ttg gtc atc gcc tgg ttt tcc ctg gtt ttg ctg 48  
 Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15  
 gca cct ccc ctc atg gcc ata tgg gaa ctg gag aaa aac gtt tat gtt 96  
 Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val  
 20 25 30  
 gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc 144  
 Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45  
 acc tgc aat act cct gaa gaa gat gac atc acc tgg acc tct gac cag 192  
 Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln  
 50 55 60  
 agc agt gaa gtc cta ggc tct ggt aaa act ctg acc atc caa gtc aaa 240  
 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
 65 70 75 80  
 gaa ttt gca gat gct ggc cag tat acc tgt cat aaa gga ggc gag gtt 288  
 Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
 85 90 95  
 ctg agc cat tcg ttc ctc ctg ata cac aaa aag gaa gat gga att tgg 336  
 Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110  
 tcc act gat atc tta agg gaa cag aaa gaa tcc aaa aat aag atc ttt 384  
 Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125  
 cta aaa tgt gag gca aag aat tat tct gga cgt ttc acc tgc tgg tgg 432  
 Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140  
 ctg acg gca atc agt acc gat ttg aaa ttc act gtc aaa agc agc aga 480  
 Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
 145 150 155 160  
 ggc tcc tct gac ccc caa ggg gtg act tgt gga gca gcg aca ctc tca 528  
 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
 165 170 175  
 gca gag aag gtc aga gtg gac aac agg gat tat aag aag tac aca gtg 576  
 Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
 180 185 190  
 gag tgt cag gag ggc agt gcc tgc ccg gct gcc gag gag agc cta ccc 624  
 Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
 195 200 205

att gaa gtc gtg gtg gac gct att cac aag ctc aag tac gaa aac tac	672
Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr	
210 215 220	

acc agc agc ttc ttc atc agg gac atc atc aaa ccg gac cca ccc aag	720
Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys	
225 230 235 240	

aac ctg caa ctg aag cca tta aaa aat tct cgg cat gtg gaa gtg agc	768
Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser	
245 250 255	

tgg gaa tac cct gac acc tgg agc acc cca cat tcc tac ttc tcc tta	816
Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu	
260 265 270	

aca ttt ggc gta cag gtc cag ggc aag aac aac aga gaa aag aaa gac	864
Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp	
275 280 285	

aga ctc tcc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat	912
Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp	
290 295 300	

gcc aag atc cgc gtg caa gcc aga gac cgc tac tat agc tca tcc tgg	960
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp	
305 310 315 320	

agc aac tgg gca tcc gtg tcc tgc a	985
Ser Asn Trp Ala Ser Val Ser Cys	
325	

<210> 56  
 <211> 328  
 <212> PRT  
 <213> Felis catus

<400> 56

Met His Pro Gln Gln Leu Val Ile Ala Trp Phe Ser Leu Val Leu Leu
1 5 10 15

Ala Pro Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asn Val Tyr Val
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu
35 40 45

Thr Cys Asn Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Asp Gln
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Ala Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val  
85 90 95

Leu Ser His Ser Phe Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Arg Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Thr Val Lys Ser Ser Arg  
145 150 155 160

Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser  
165 170 175

Ala Glu Lys Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Gly Val Gln Val Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Ser Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290

295

300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

Ser Asn Trp Ala Ser Val Ser Cys  
 325

<210> 57  
 <211> 985  
 <212> DNA  
 <213> Felis catus

<400> 57  
 tgcaggacac ggatgccag ttgctccagg atgagctata gtagcggctct ctggcttgca 60  
 cgcggatcctt ggcatccttg tggcacacga ccttggtgta ggtcttgctc acggagagtc 120  
 tgtctttctt ttctctgttg ttcttgccct ggacctgtac gccaaatgtt aaggagaagt 180  
 aggaatgtgg ggtgctccag gtgtcagggg attcccagct cacttccaca tgccgagaat 240  
 tttttaatgg cttcagttgc aggttcttgg gtgggtccgg tttgatgatg tccctgatga 300  
 agaagctgct ggtgtagttt tcgtacttga gcttgtgaat agcgtccacc acgacttcaa 360  
 tgggtaggct ctctcggca gccgggcagg cactgccttc ctgacactcc actgtgtact 420  
 tcttataatc cctgttgctc actctgacct tctctgctga gagtgtcgt gctccacaag 480  
 tcacccttg ggggtcagag gagcctctgc tgcttttgac agtgaatttc aaatcgggtac 540  
 tgattgccgt cagccaccag caggtgaaac gtccagaata attctttgcc tcacatttta 600  
 gaaagatcctt atttttggat tctttctgtt cccttaagat atcagtggac caaattccat 660  
 cttccttttt gtgtatcagg aggaacgaat ggctcagaac ctgcctcct ttatgacagg 720  
 tatactggcc agcatctgca aattctttga cttggatggt cagagtttta ccagagccta 780  
 ggacttcact gctctggtca gaggtccagg tgatgtcatc ttcttcagga gtattgcagg 840  
 tgaggaccac catttctccg ggggcatcag ggtgccagtc caactctaca acataaacgt 900  
 ttttctccag ttcccatatg gccatgaggg gaggtgccag caaaaccagg gaaaaccagg 960  
 cgatgaccaa ctgctgagga tgcatt 985

<210> 58  
 <211> 987  
 <212> DNA  
 <213> Canis familiaris



<220>  
 <221> CDS  
 <222> (1)..(987)

<400> 58

atg cac cct cag cag ttg gtc atc tcc tgg ttt tcc ctc gtt ttg ctg	48
Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu	
1 5 10 15	

gcg tct ccc ctc atg gcc ata tgg gaa ctg gag aaa gat gtt tat gtt	96
Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val	
20 25 30	

gta gag ttg gac tgg cac cct gat gcc ccc gga gaa atg gtg gtc ctc	144
Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu	
35 40 45	

acc tgc cat acc cct gaa gaa gat gac atc act tgg acc tca gcg cag	192
Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln	
50 55 60	

agc agt gaa gtc cta ggt tct ggt aaa act ctg acc atc caa gtc aaa	240
Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys	
65 70 75 80	

gaa ttt gga gat gct ggc cag tat acc tgc cat aaa gga ggc aag gtt	288
Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val	
85 90 95	

ctg agc cgc tca ctc ctg ttg att cac aaa aaa gaa gat gga att tgg	336
Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp	
100 105 110	

tcc act gat atc tta aag gaa cag aaa gaa tcc aaa aat aag atc ttt	384
Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe	
115 120 125	

ctg aaa tgt gag gca aag aat tat tct gga cgt ttc aca tgc tgg tgg	432
Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp	
130 135 140	

ctg acg gca atc agt act gat ttg aaa ttc agt gtc aaa agt agc aga	480
Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg	
145 150 155 160	

ggc ttc tct gac ccc caa ggg gtg aca tgt gga gca gtg aca ctt tca	528
Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser	
165 170 175	

gca gag agg gtc aga gtg gac aac agg gat tat aag aag tac aca gtg	576
Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val	
180 185 190	

gag tgt cag gag ggc agt gcc tgc ccc tct gcc gag gag agc cta ccc	624
Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro	
195 200 205	

atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac 672  
 Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
 210 215 220

acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca 720  
 Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
 225 230 235 240

aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc 768  
 Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
 245 250 255

tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg 816  
 Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
 260 265 270

aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat 864  
 Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
 275 280 285

aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat 912  
 Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
 290 295 300

gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg 960  
 Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320

agc gac tgg gca tct gtg tca tgc agt 987  
 Ser Asp Trp Ala Ser Val Ser Cys Ser  
 325

<210> 59  
 <211> 329  
 <212> PRT  
 <213> Canis familiaris

<400> 59

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu  
 1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
 20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
 35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
 50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
85 90 95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp

290	295	300
Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp		
305	310	315 320

Ser Asp Trp Ala Ser Val Ser Cys Ser  
325

<210> 60  
<211> 987  
<212> DNA  
<213> Canis familiaris

<400> 60	
actgcatgac acagatgccc agtcgctcca ggatgaacta tagtagcggg ctcgggcttg	60
cacgcggatc ttggcatcct tgtggcacac gaccttggct gaggtccttg ccacgcagag	120
tctatctttc ttttctctat tgttcttgcc ctgggcctgt atgcaaaatg tcaggagaaa	180
gtaggaatgt ggggtgctcc aggtgtcggg gtattcccag ctgacctcca cgtgccgaga	240
atctttcaat ggcttcagct gcaggtttgt ggggtgggtct ggtttgatga tgtctctgat	300
gaagaagctg ctggtgtagt tttcatactt gagcttgtga atagcatcca ccacgacctc	360
gatgggtagg ctctcctcgg cagaggggca ggcactgccc tctgacact ccactgtgta	420
cttcttataa tccctgttgt ccactctgac cctctctgct gaaagtgtca ctgctccaca	480
tgtcaccctt tgggggtcag agaagcctct gctacttttg aactgaatt tcaaatcagt	540
actgattgcc gtcagccacc agcatgtgaa acgtccagaa taattctttg cctcacattt	600
cagaaagatc ttatttttgg attctttctg ttcctttaag atatcagtgg accaaattcc	660
atcttctttt ttgtgaatca acaggagtga gcggtcaga accttgacct ctttatggca	720
ggtatactgg ccagcatctc caaattcttt gacttggatg gtcagagttt taccagaacc	780
taggacttca ctgctctgcg ctgaggcca agtgatgtca tcttcttcag gggatatggca	840
ggtgaggacc accatttctc cgggggcac agggtgccag tccaactcta caacataaac	900
atctttctcc agttcccata tggccatgag gggagacgcc agcaaacga gggaaaacca	960
ggagatgacc aactgctgag ggtgcat	987

<210> 61  
<211> 1599  
<212> DNA  
<213> Canis familiaris

<220>

<221> CDS

<222> (1)..(1599)

<400> 61

atg	cac	cct	cag	cag	ttg	gtc	atc	tcc	tgg	ttt	tcc	ctc	ggt	ttg	ctg	48
Met	His	Pro	Gln	Gln	Leu	Val	Ile	Ser	Trp	Phe	Ser	Leu	Val	Leu	Leu	
1			5					10					15			

gcg	tct	ccc	ctc	atg	gcc	ata	tgg	gaa	ctg	gag	aaa	gat	ggt	tat	ggt	96
Ala	Ser	Pro	Leu	Met	Ala	Ile	Trp	Glu	Leu	Glu	Lys	Asp	Val	Tyr	Val	
			20					25					30			

gta	gag	ttg	gac	tgg	cac	cct	gat	gcc	ccc	gga	gaa	atg	gtg	gtc	ctc	144
Val	Glu	Leu	Asp	Trp	His	Pro	Asp	Ala	Pro	Gly	Glu	Met	Val	Val	Leu	
		35					40					45				

acc	tgc	cat	acc	cct	gaa	gaa	gat	gac	atc	act	tgg	acc	tca	gcg	cag	192
Thr	Cys	His	Thr	Pro	Glu	Glu	Asp	Asp	Ile	Thr	Trp	Thr	Ser	Ala	Gln	
	50						55				60					

agc	agt	gaa	gtc	cta	ggg	tct	ggg	aaa	act	ctg	acc	atc	caa	gtc	aaa	240
Ser	Ser	Glu	Val	Leu	Gly	Ser	Gly	Lys	Thr	Leu	Thr	Ile	Gln	Val	Lys	
65					70				75						80	

gaa	ttt	gga	gat	gct	ggc	cag	tat	acc	tgc	cat	aaa	gga	ggc	aag	ggt	288
Glu	Phe	Gly	Asp	Ala	Gly	Gln	Tyr	Thr	Cys	His	Lys	Gly	Gly	Lys	Val	
				85					90					95		

ctg	agc	cgc	tca	ctc	ctg	ttg	att	cac	aaa	aaa	gaa	gat	gga	att	tgg	336
Leu	Ser	Arg	Ser	Leu	Leu	Leu	Ile	His	Lys	Lys	Glu	Asp	Gly	Ile	Trp	
			100					105					110			

tcc	act	gat	atc	tta	aag	gaa	cag	aaa	gaa	tcc	aaa	aat	aag	atc	ttt	384
Ser	Thr	Asp	Ile	Leu	Lys	Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	
		115					120					125				

ctg	aaa	tgt	gag	gca	aag	aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	432
Leu	Lys	Cys	Glu	Ala	Lys	Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	
	130					135					140					

ctg	acg	gca	atc	agt	act	gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	480
Leu	Thr	Ala	Ile	Ser	Thr	Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	
145					150					155					160	

ggc	ttc	tct	gac	ccc	caa	ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	528
Gly	Phe	Ser	Asp	Pro	Gln	Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	
				165					170					175		

gca	gag	agg	gtc	aga	gtg	gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	576
Ala	Glu	Arg	Val	Arg	Val	Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	
			180					185					190			

gag	tgt	cag	gag	ggc	agt	gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	624
Glu	Cys	Gln	Glu	Gly	Ser	Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	
		195					200					205				

atc gag gtc gtg gtg gat gct att cac aag ctc aag tat gaa aac tac Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr 210 215 220	672
acc agc agc ttc ttc atc aga gac atc atc aaa cca gac cca ccc aca Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr 225 230 235 240	720
aac ctg cag ctg aag cca ttg aaa aat tct cgg cac gtg gag gtc agc Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser 245 250 255	768
tgg gaa tac ccc gac acc tgg agc acc cca cat tcc tac ttc tcc ctg Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu 260 265 270	816
aca ttt tgc ata cag gcc cag ggc aag aac aat aga gaa aag aaa gat Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp 275 280 285	864
aga ctc tgc gtg gac aag acc tca gcc aag gtc gtg tgc cac aag gat Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp 290 295 300	912
gcc aag atc cgc gtg caa gcc cga gac cgc tac tat agt tca tcc tgg Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp 305 310 315 320	960
agc gac tgg gca tct gtg tca tgc agt ggt ggc ggt ggc ggc gga tct Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser 325 330 335	1008
aga aac ttg cca acc cct act cca tcc ccg ggt atg ttc caa tgt ttg Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu 340 345 350	1056
aac cac tcc caa acc ttg ttg aga gcc gtc agc aac acg ctt cag aag Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys 355 360 365	1104
gcc aga caa act cta gaa tta tat tcc tgc act tcc gaa gag att gat Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp 370 375 380	1152
cat gaa gat atc aca aag gat aaa acc agc aca gtg gag gcc tgc tta His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu 385 390 395 400	1200
cca ctg gaa tta acc atg aat gag agt tgc ctg gct tcc aga gag atc Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile 405 410 415	1248
tct ttg ata act aac ggg agt tgc ctg gcc tct gga aag gcc tct ttt Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe 420 425 430	1296

atg acg gtc ctg tgc ctt agc agc atc tat gag gac ttg aag atg tac 1344  
Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
435 440 445

cag atg gaa ttc aag gcc atg aac gca aag ctt tta atg gat ccc aag 1392  
Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
450 455 460

agg cag atc ttt ctg gat caa aac atg ctg aca gct atc gat gag ctg 1440  
Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
465 470 475 480

tta cag gcc ctg aat ttc aac agt gtg act gtg cca cag aaa tcc tcc 1488  
Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser  
485 490 495

ctt gaa gag ccg gat ttt tat aaa act aaa atc aag ctc tgc ata ctt 1536  
Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
500 505 510

ctt cat gct ttc aga att cgt gcg gtg acc atc aat aga atg atg tcc 1584  
Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
515 520 525

tac ttg aac tct tcc 1599  
Tyr Leu Asn Ser Ser  
530

<210> 62  
<211> 533  
<212> PRT  
<213> Canis familiaris

<400> 62

Met His Pro Gln Gln Leu Val Ile Ser Trp Phe Ser Leu Val Leu Leu  
1 5 10 15

Ala Ser Pro Leu Met Ala Ile Trp Glu Leu Glu Lys Asp Val Tyr Val  
20 25 30

Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
35 40 45

Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
50 55 60

Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
65 70 75 80

Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val

85

90

95

Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
 100 105 110

Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
 115 120 125

Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
 130 135 140

Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
 145 150 155 160

Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
 165 170 175

Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
 180 185 190

Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
 195 200 205

Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
 210 215 220

Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
 225 230 235 240

Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
 245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu  
 260 265 270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
 275 280 285

Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
 290 295 300

Ala Lys Ile Arg Val Gln Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp  
 305 310 315 320



Ser Asp Trp Ala Ser Val Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser  
 325 330 335

Arg Asn Leu Pro Thr Pro Thr Pro Ser Pro Gly Met Phe Gln Cys Leu  
 340 345 350

Asn His Ser Gln Thr Leu Leu Arg Ala Val Ser Asn Thr Leu Gln Lys  
 355 360 365

Ala Arg Gln Thr Leu Glu Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp  
 370 375 380

His Glu Asp Ile Thr Lys Asp Lys Thr Ser Thr Val Glu Ala Cys Leu  
 385 390 395 400

Pro Leu Glu Leu Thr Met Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile  
 405 410 415

Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe  
 420 425 430

Met Thr Val Leu Cys Leu Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr  
 435 440 445

Gln Met Glu Phe Lys Ala Met Asn Ala Lys Leu Leu Met Asp Pro Lys  
 450 455 460

Arg Gln Ile Phe Leu Asp Gln Asn Met Leu Thr Ala Ile Asp Glu Leu  
 465 470 475 480

Leu Gln Ala Leu Asn Phe Asn Ser Val Thr Val Pro Gln Lys Ser Ser  
 485 490 495

Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu  
 500 505 510

Leu His Ala Phe Arg Ile Arg Ala Val Thr Ile Asn Arg Met Met Ser  
 515 520 525

Tyr Leu Asn Ser Ser  
 530

<210> 63  
 <211> 1599  
 <212> DNA  
 <213> Canis familiaris

<400> 63  
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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120  
 ctgtggcaca gtcacactgt tgaaattcag ggccctgtaac agctcatcga tagctgtcag 180  
 catgtttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240  
 cttgaattcc atctggtaca tcttcaagtc ctcatagatg ctgctaaggc acaggaccgt 300  
 cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360  
 ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct 420  
 ggttttatcc tttgtgatat cttcatgac aatctcttcg gaagtgcagg aatataattc 480  
 tagagtttgt ctggccttct gaagcgtggt gctgacggct ctcaacaagg tttgggagtg 540  
 gttcaaakat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600  
 gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660  
 gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720  
 gtccacgcag agtctatctt tcttttctct attgttcttg ccctgggcct gtatgcaaaa 780  
 tgtcagggag aagtaggaat gtggggtgct ccaggtgtcg gggatttccc agctgacctc 840  
 cacgtgccga gaatTTTTCA atggcttcag ctgcagggtt gtgggtgggt ctggtttgat 900  
 gatgtctctg atgaagaagc tgctgggtga gttttcatac ttgagcttgt gaatagcatc 960  
 caccacgacc tcgatgggta ggctctctc ggagagggg caggcactgc cctcctgaca 1020  
 ctccactgtg tacttcttat aatccctgtt gtccactctg accctctctg ctgaaagtgt 1080  
 cactgctcca catgtcaccc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140  
 tttcaaatca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200  
 tgccctcatat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt 1260  
 ggaccaaatt ccatcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc 1320  
 tcctttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt 1380  
 tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc 1440  
 aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc 1500

tacaacataa acatctttct ccagttccca tatggccatg aggggagacg ccagcaaaac 1560

gagggaaaac caggagatga ccaactgctg aggggtgcat 1599

<210> 64  
<211> 0  
<212> DNA  
<213> Canis familiaris

<400> 64  
000

<210> 65  
<211> 0  
<212> DNA  
<213> Canis familiaris

<400> 65  
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<210> 66  
<211> 1533  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (1)..(1533)

<400> 66  
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Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His  
1 5 10 15

cct gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa 96  
Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu  
20 25 30

gaa gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt 144  
Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly  
35 40 45

tct ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc 192  
Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly  
50 55 60

cag tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg 240  
Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu  
65 70 75 80

ttg att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag 288  
Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys  
85 90 95

gaa cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag 336

Glu	Gln	Lys	Glu	Ser	Lys	Asn	Lys	Ile	Phe	Leu	Lys	Cys	Glu	Ala	Lys		
			100					105					110				
aat	tat	tct	gga	cgt	ttc	aca	tgc	tgg	tgg	ctg	acg	gca	atc	agt	act	384	
Asn	Tyr	Ser	Gly	Arg	Phe	Thr	Cys	Trp	Trp	Leu	Thr	Ala	Ile	Ser	Thr		
		115					120					125					
gat	ttg	aaa	ttc	agt	gtc	aaa	agt	agc	aga	ggc	ttc	tct	gac	ccc	caa	432	
Asp	Leu	Lys	Phe	Ser	Val	Lys	Ser	Ser	Arg	Gly	Phe	Ser	Asp	Pro	Gln		
	130					135					140						
ggg	gtg	aca	tgt	gga	gca	gtg	aca	ctt	tca	gca	gag	agg	gtc	aga	gtg	480	
Gly	Val	Thr	Cys	Gly	Ala	Val	Thr	Leu	Ser	Ala	Glu	Arg	Val	Arg	Val		
145					150					155					160		
gac	aac	agg	gat	tat	aag	aag	tac	aca	gtg	gag	tgt	cag	gag	ggc	agt	528	
Asp	Asn	Arg	Asp	Tyr	Lys	Lys	Tyr	Thr	Val	Glu	Cys	Gln	Glu	Gly	Ser		
				165				170						175			
gcc	tgc	ccc	tct	gcc	gag	gag	agc	cta	ccc	atc	gag	gtc	gtg	gtg	gat	576	
Ala	Cys	Pro	Ser	Ala	Glu	Glu	Ser	Leu	Pro	Ile	Glu	Val	Val	Val	Asp		
			180					185					190				
gct	att	cac	aag	ctc	aag	tat	gaa	aac	tac	acc	agc	agc	ttc	ttc	atc	624	
Ala	Ile	His	Lys	Leu	Lys	Tyr	Glu	Asn	Tyr	Thr	Ser	Ser	Phe	Phe	Ile		
		195				200						205					
aga	gac	atc	atc	aaa	cca	gac	cca	ccc	aca	aac	ctg	cag	ctg	aag	cca	672	
Arg	Asp	Ile	Ile	Lys	Pro	Asp	Pro	Pro	Thr	Asn	Leu	Gln	Leu	Lys	Pro		
	210					215					220						
ttg	aaa	aat	tct	cgg	cac	gtg	gag	gtc	agc	tgg	gaa	tac	ccc	gac	acc	720	
Leu	Lys	Asn	Ser	Arg	His	Val	Glu	Val	Ser	Trp	Glu	Tyr	Pro	Asp	Thr		
225					230				235						240		
tgg	agc	acc	cca	cat	tcc	tac	ttc	tcc	ctg	aca	ttt	tgc	ata	cag	gcc	768	
Trp	Ser	Thr	Pro	His	Ser	Tyr	Phe	Ser	Leu	Thr	Phe	Cys	Ile	Gln	Ala		
				245				250						255			
cag	ggc	aag	aac	aat	aga	gaa	aag	aaa	gat	aga	ctc	tgc	gtg	gac	aag	816	
Gln	Gly	Lys	Asn	Asn	Arg	Glu	Lys	Lys	Asp	Arg	Leu	Cys	Val	Asp	Lys		
			260				265					270					
acc	tca	gcc	aag	gtc	gtg	tgc	cac	aag	gat	gcc	aag	atc	cgc	gtg	caa	864	
Thr	Ser	Ala	Lys	Val	Val	Cys	His	Lys	Asp	Ala	Lys	Ile	Arg	Val	Gln		
		275				280						285					
gcc	cga	gac	cgc	tac	tat	agt	tca	tcc	tgg	agc	gac	tgg	gca	tct	gtg	912	
Ala	Arg	Asp	Arg	Tyr	Tyr	Ser	Ser	Ser	Trp	Ser	Asp	Trp	Ala	Ser	Val		
	290					295					300						
tca	tgc	agt	ggc	ggc	ggc	ggc	gga	tct	aga	aac	ttg	cca	acc	cct		960	
Ser	Cys	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Arg	Asn	Leu	Pro	Thr	Pro		
305					310				315					320			
act	cca	tcc	ccg	ggc	atg	ttc	caa	tgt	ttg	aac	cac	tcc	caa	acc	ttg	1008	
Thr	Pro	Ser	Pro	Gly	Met	Phe	Gln	Cys	Leu	Asn	His	Ser	Gln	Thr	Leu		

	325	330	335	
ttg aga gcc gtc agc aac acg ctt cag aag gcc aga caa act cta gaa				1056
Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu				
	340	345	350	
tta tat tcc tgc act tcc gaa gag att gat cat gaa gat atc aca aag				1104
Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys				
	355	360	365	
gat aaa acc agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg				1152
Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met				
	370	375	380	
aat gag agt tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg				1200
Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly				
	385	390	395	400
agt tgc ctg gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt				1248
Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu				
	405	410	415	
agc agc atc tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc				1296
Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala				
	420	425	430	
atg aac gca aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat				1344
Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp				
	435	440	445	
caa aac atg ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc				1392
Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe				
	450	455	460	
aac agt gtg act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt				1440
Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe				
	465	470	475	480
tat aaa act aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att				1488
Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile				
	485	490	495	
cgt gcg gtg acc atc aat aga atg atg tcc tac ttg aac tct tcc				1533
Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser				
	500	505	510	

<210> 67  
 <211> 511  
 <212> PRT  
 <213> Canis familiaris

<400> 67

Ile Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His
1 5 10 15

Pro Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu  
 20 25 30

Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly  
 35 40 45

Ser Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly  
 50 55 60

Gln Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu  
 65 70 75 80

Leu Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys  
 85 90 95

Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys  
 100 105 110

Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr  
 115 120 125

Asp Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln  
 130 135 140

Gly Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val  
 145 150 155 160

Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser  
 165 170 175

Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp  
 180 185 190

Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile  
 195 200 205

Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro  
 210 215 220

Leu Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr  
 225 230 235 240

Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala  
245 250 255

Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys  
260 265 270

Thr Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln  
275 280 285

Ala Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val  
290 295 300

Ser Cys Ser Gly Gly Gly Gly Gly Gly Ser Arg Asn Leu Pro Thr Pro  
305 310 315 320

Thr Pro Ser Pro Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu  
325 330 335

Leu Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu  
340 345 350

Leu Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys  
355 360 365

Asp Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met  
370 375 380

Asn Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly  
385 390 395 400

Ser Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu  
405 410 415

Ser Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala  
420 425 430

Met Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp  
435 440 445

Gln Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe  
450 455 460

Asn Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe

465

470

475

480

Tyr Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile  
 485 490 495

Arg Ala Val Thr Ile Asn Arg Met Met Ser Tyr Leu Asn Ser Ser  
 500 505 510

&lt;210&gt; 68

&lt;211&gt; 1533

&lt;212&gt; DNA

&lt;213&gt; Canis familiaris

&lt;400&gt; 68

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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggctcttcaa gggaggattt 120  
 ctgtggcaca gtcacactgt tgaaattcag ggctgtaac agctcatcga tagctgtcag 180  
 catgttttga tccagaaaga tctgcctctt gggatccatt aaaagctttg cgttcatggc 240  
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 cataaaagag gcctttccag aggccaggca actcccgtta gttatcaaag agatctctct 360  
 ggaagccagg caactctcat tcatgggttaa ttccagtggg aagcaggcct ccactgtgct 420  
 ggttttatcc tttgtgatat cttcatgac aatctcttcg gaagtgcagg aatataattc 480  
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 gttcaaacat tggaacatac ccggggatgg agtaggggtt ggcaagtttc tagatccgcc 600  
 gccaccgcca ccactgcatg acacagatgc ccagtcgctc caggatgaac tatagtagcg 660  
 gtctcgggct tgcacgcgga tcttggcatc cttgtggcac acgaccttgg ctgaggtctt 720  
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 cacgtgccga gaatttttca atggcttcag ctgcagggtt gtgggtgggt ctggtttgat 900  
 gatgtctctg atgaagaagc tgctgggtgta gttttcatac ttgagcttgt gaatagcatc 960  
 caccacgacc tcgatgggta ggctctcctc ggcagagggg caggcactgc cctcctgaca 1020  
 ctccactgtg tacttcttat aatccctggt gtccactctg accctctctg ctgaaagtgt 1080  
 cactgctcca catgtcacc cttgggggtc agagaagcct ctgctacttt tgacactgaa 1140  
 tttcaaatca gtactgattg ccgtcagcca ccagcatgtg aaacgtccag aataattctt 1200



tgccctcacat ttcagaaaga tcttattttt ggattctttc tgttccttta agatatcagt	1260
ggaccaaatt ccatcttctt ttttgtgaat caacaggagt gagcggctca gaaccttgcc	1320
tccttttatgg caggtatact ggccagcatc tccaaattct ttgacttgga tggtcagagt	1380
tttaccagaa cctaggactt cactgctctg cgctgaggtc caagtgatgt catcttcttc	1440
aggggtatgg caggtgagga ccaccatttc tccgggggca tcagggtgcc agtccaactc	1500
tacaacataa acatctttct ccagttccca tat	1533

<210> 69  
 <211> 30  
 <212> DNA  
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<220>  
 <223> Synthetic Primer

<400> 69	
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<210> 70  
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 <212> DNA  
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<220>  
 <223> Synthetic Primer

<400> 70	
cgacggccag tgaattgtaa tacgactc	28

<210> 71  
 <211> 31  
 <212> DNA  
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<220>  
 <223> Synthetic Primer

<400> 71	
agtgatgaag gcctggaatc agattacttt g	31

<210> 72  
 <211> 32  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Primer

<400> 72  
 atggcctgga acacttctct gaaagaatat ga 32

<210> 73  
 <211> 30  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> Synthetic Primer

<400> 73  
 aactattgag cacagggata aagatgactg 30

<210> 74  
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 <212> DNA  
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<220>  
 <223> Synthetic Primer

<400> 74  
 aatatctaatt tcttgttttg aacagtgaac att 33

<210> 75  
 <211> 36  
 <212> DNA  
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<220>  
 <223> Synthetic Primer

<400> 75  
 tatgccggct actttggcaa gcttgaacat aaactc 36

<210> 76  
 <211> 37  
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<220>  
 <223> Synthetic Primer

<400> 76  
 ggcctcgagc taattcttgt tttgaacagt gaacatt 37

<210> 77  
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 atggccgaca aggtcctgaa ggagaaga 28  
  
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 <400> 78  
 ttaatgtcct gggaagaggt agaaacatct tgt 33  
  
 <210> 79  
 <211> 26  
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 <220>  
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 <400> 80  
 ctggagagtc actgatcaac agttcc 26  
  
 <210> 81  
 <211> 36  
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 <400> 81  
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 <210> 82  
 <211> 39

<212> DNA  
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 <400> 82  
 cgcctctaga cctcaattgc caggaagag atagaagta 39  
  
 <210> 83  
 <211> 60  
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 <220>  
 <223> Synthetic Primer  
  
 <400> 83  
 ctgcagtggg gccgggtggcg gcggatctag aaacttgcca accctactc catccccggg 60  
  
 <210> 84  
 <211> 60  
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 <220>  
 <223> Synthetic Primer  
  
 <400> 84  
 cccggggatg gagtaggggt tggcaagttt ctagatccgc cgccaccgcc accactgcag 60  
  
 <210> 85  
 <211> 28  
 <212> DNA  
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 <220>  
 <223> Synthetic Primer  
  
 <400> 85  
 atgcatcctc agcagttggt catgcct 28  
  
 <210> 86  
 <211> 25  
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 <223> Synthetic Primer  
  
 <400> 86  
 tgcaggacac ggatgccag ttgct 25

<210> 87  
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 <400> 87  
 acaggtacca tgcatacctca gcagttgggc atcgccct 37  
  
 <210> 88  
 <211> 25  
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 <213> Artificial sequence  
  
 <220>  
 <223> Synthetic Primer  
  
 <400> 88  
 ctaactgcag gacacggatg cccag 25  
  
 <210> 89  
 <211> 19  
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 <400> 89  
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<400> 91  
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<210> 92  
 <211> 41  
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<220>  
 <223> Synthetic Primer

<400> 92  
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<210> 93  
 <211> 20  
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<220>  
 <223> Synthetic Primer

<400> 93  
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<210> 94  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Synthetic Primer

<400> 94  
 ccatctggta catcttcaag tc 22

<210> 95  
 <211> 38  
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<220>  
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<400> 95  
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<210> 96  
 <211> 51  
 <212> DNA  
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<220>  
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 <400> 96  
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 <210> 97  
 <211> 22  
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 <400> 97  
 cttaaaggaa cagaaagaat cc 22  
  
 <210> 98  
 <211> 19  
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 ggtattccca gctgacctc 19  
  
 <210> 99  
 <211> 37  
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 <223> Synthetic Primer  
  
 <400> 99  
 cataggtacc atgcaccctc agcagttggt catctcc 37  
  
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 <211> 29  
 <212> DNA  
 <213> Artificial sequence  
  
 <220>  
 <223> Synthetic Primer  
  
 <400> 100  
 atctaaatgc atgacacaga tgcccagtc 29  
  
 <210> 101  
 <211> 561

<212> DNA  
 <213> Felis catus

<220>  
 <221> CDS  
 <222> (1)..(561)

<400> 101  
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 Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile  
 1 5 10 15  
 agc aac acg ctt cag aag gcc aga caa act cta gaa ttt tac tcc tgc 96  
 Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys  
 20 25 30  
 act tcc gaa gag att gat cat gaa gat atc aca aaa gat aaa acc agc 144  
 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser  
 35 40 45  
 aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt tgc 192  
 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys  
 50 55 60  
 ctg gct tcc aga gag atc tct ctg ata act aat ggg agt tgc ctg gcc 240  
 Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala  
 65 70 75 80  
 tcc aga aag acc tct ttt atg acg acc ctg tgc ctt agc agt atc tat 288  
 Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr  
 85 90 95  
 gag gac ttg aag atg tac cag gtg gag ttc aag gcc atg aat gca aag 336  
 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys  
 100 105 110  
 ctg tta atg gat cct aaa agg cag atc ttt ctg gat caa aac atg ctg 384  
 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu  
 115 120 125  
 aca gct att gat gag ctg tta cag gcc ctg aat gtc aac agt gtg act 432  
 Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr  
 130 135 140  
 gtg cca cag aac tcc tcc ctg gaa gaa ccg gat ttt tat aaa act aaa 480  
 Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys  
 145 150 155 160  
 atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gca gtg acc 528  
 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr  
 165 170 175  
 atc aat aga atg atg agc tat ctg aat gct tcc 561  
 Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
 180 185



<210> 102  
 <211> 187  
 <212> PRT  
 <213> Felis catus

<400> 102

Gly Met Phe Gln Cys Leu Asn His Ser Gln Thr Leu Leu Arg Ala Ile  
 1 5 10 15

Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Ser Cys  
 20 25 30

Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser  
 35 40 45

Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser Cys  
 50 55 60

Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu Ala  
 65 70 75 80

Ser Arg Lys Thr Ser Phe Met Thr Thr Leu Cys Leu Ser Ser Ile Tyr  
 85 90 95

Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Ala Met Asn Ala Lys  
 100 105 110

Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu  
 115 120 125

Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Val Asn Ser Val Thr  
 130 135 140

Val Pro Gln Asn Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys  
 145 150 155 160

Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr  
 165 170 175

Ile Asn Arg Met Met Ser Tyr Leu Asn Ala Ser  
 180 185

<210> 103

<211> 561  
 <212> DNA  
 <213> Felis catus

<400> 103  
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 aagaagtatg cagagcttga ttttagtttt ataaaaatcc ggttcttcca gggaggagtt 120  
 ctgtggcaca gtcacactgt tgacattcag ggctgtaac agctcatcaa tagctgtcag 180  
 catgttttga tccagaaaga tctgcctttt aggatccatt aacagctttg cattcatggc 240  
 cttgaactcc acctggtaca tcttcaagtc ctcatagata ctgctaaggc acagggtcgt 300  
 cataaaagag gtcttttctgg aggccaggca actcccatta gttatcagag agatctctct 360  
 ggaagccagg caactctcat tcatggttaa ttccagtggc aagcaggcct ccactgtgct 420  
 ggttttatct tttgtgatat cttcatgatc aatctcttcg gaagtgcagg agtaaaattc 480  
 tagagtttgt ctggccttct gaagcgtggt gctgatggct cgcagcaggg tttgggagtg 540  
 gttgaggcac tggaacatcc c 561

<210> 104  
 <211> 1455  
 <212> DNA  
 <213> Canis familiaris

<220>  
 <221> CDS  
 <222> (232)..(897)

<400> 104  
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 agacagagag agaaagcaag ccggacaccg gaggcccgga aaagtccctg cgcgccctcg 120  
 gccattata aaaatgtgac cccccgggtc ggctccccc cgccgccctc cctgcccgcg 180  
 tccgcagtcc gcgtccagcg cccgcggggg tccacgcagc gcccgcccag c atg tgc 237  
 Met Cys  
 1  
 ccg ccg cgc ggc ctc ctc ctt gtg acc atc ctg gtc ctg cta agc cac 285  
 Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu Ser His  
 5 10 15  
 ctg gac cac ctt act tgg gcc agg agc ctc ccc aca gcc tca ccg agc 333  
 Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser Pro Ser  
 20 25 30  
 cca gga ata ttc cag tgc ctc aac cac tcc caa aac ctg ctg aga gcc 381  
 Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu Arg Ala

35	40	45	50	
gtc agc aac acg ctt cag aag gcc aga caa act cta gaa tta tat tcc				429
Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu Tyr Ser	55	60	65	
tgc act tcc gaa gag att gat cat gaa gat atc aca aag gat aaa acc				477
Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr	70	75	80	
agc aca gtg gag gcc tgc tta cca ctg gaa tta acc atg aat gag agt				525
Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn Glu Ser	85	90	95	
tgc ctg gct tcc aga gag atc tct ttg ata act aac ggg agt tgc ctg				573
Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser Cys Leu	100	105	110	
gcc tct gga aag gcc tct ttt atg acg gtc ctg tgc ctt agc agc atc				621
Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser Ser Ile	115	120	125	130
tat gag gac ttg aag atg tac cag atg gaa ttc aag gcc atg aac gca				669
Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met Asn Ala	135	140	145	
aag ctt tta atg gat ccc aag agg cag atc ttt ctg gat caa aac atg				717
Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met	150	155	160	
ctg aca gct atc gat gag ctg tta cag gcc ctg aat ttc aac agt gtg				765
Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn Ser Val	165	170	175	
act gtg cca cag aaa tcc tcc ctt gaa gag ccg gat ttt tat aaa act				813
Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr	180	185	190	
aaa atc aag ctc tgc ata ctt ctt cat gct ttc aga att cgt gcg gtg				861
Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val	195	200	205	210
acc atc gat aga atg atg agt tat ctg aat tct tcc taaaaagctg				907
Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser	215	220		
aggtctctct cgactttaaa gtcattccta taaaaatgtg aaccctaaag aatttttcat				967
aagatagggg ttaagaacca gggaggggggt ggcttgacct ggtcctactt aagctagtac				1027
gataattctc atgcttggtt acattagttg ccactcaaatt tttgaaagat gtgactgtta				1087
tatccacac gatgcctttg accaagtata tttcacattt actatggata agttaagtgt				1147
tcgtgagcaa attgctaaag aggaaaaatg tcctcaccga acatgttttt attttccctt				1207
taatagaaga gcaagacttt ataagctatt tctgtaccaa actgtttgtg gaaacaaaca				1267

ctcaagcata atttatttaa aaatacttat ttatataatt ttgtgttcat gaaagcatgt 1327  
gaattaatuu atatttatuu atgttatatt tattaaagta tttattatca agtggatttg 1387  
ggatatctta tgttctaaaa ataaaatgat tgagtagaaa aaaaaaaaaa aaaaaaaaaa 1447  
aaaaaaaaa 1455

<210> 105  
<211> 222  
<212> PRT  
<213> Canis familiaris  
<400> 105

Met Cys Pro Pro Arg Gly Leu Leu Leu Val Thr Ile Leu Val Leu Leu  
1 5 10 15

Ser His Leu Asp His Leu Thr Trp Ala Arg Ser Leu Pro Thr Ala Ser  
20 25 30

Pro Ser Pro Gly Ile Phe Gln Cys Leu Asn His Ser Gln Asn Leu Leu  
35 40 45

Arg Ala Val Ser Asn Thr Leu Gln Lys Ala Arg Gln Thr Leu Glu Leu  
50 55 60

Tyr Ser Cys Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp  
65 70 75 80

Lys Thr Ser Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Met Asn  
85 90 95

Glu Ser Cys Leu Ala Ser Arg Glu Ile Ser Leu Ile Thr Asn Gly Ser  
100 105 110

Cys Leu Ala Ser Gly Lys Ala Ser Phe Met Thr Val Leu Cys Leu Ser  
115 120 125

Ser Ile Tyr Glu Asp Leu Lys Met Tyr Gln Met Glu Phe Lys Ala Met  
130 135 140

Asn Ala Lys Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln  
145 150 155 160

Asn Met Leu Thr Ala Ile Asp Glu Leu Leu Gln Ala Leu Asn Phe Asn  
165 170 175

Ser Val Thr Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr  
180 185 190

Lys Thr Lys Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg  
195 200 205

Ala Val Thr Ile Asp Arg Met Met Ser Tyr Leu Asn Ser Ser  
210 215 220

<210> 106  
<211> 1455  
<212> DNA  
<213> Canis familiaris

<400> 106  
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agatatccca aatccacttg ataataaata ctttaataaa tataacataa ataaatataa 120  
attaattcac atgctttcat gaacacaaaa ttatataaat aagtattttt aaataaatta 180  
tgcttgagtg tttgtttcta caaacagttt ggtacagaaa tagcttataa agtcttgctc 240  
ttctattaaa gggaaaataa aaacatgttc ggtgaggaca tttttcctct ttagcaattt 300  
gctcacgaac acttaactta tccatagtaa atgtgaaata tacttggtca aaggcatcgt 360  
gtgggatata acagtcacat ctttcaaat ttgagtggca actaatgtaa acaagcatga 420  
gaattatcgt actagcttaa gtaggaccag gtcaagccac cccctccctg gttcttaacc 480  
cctatcttat gaaaaattct tttgggttca catttttata ggaatgactt taaagtcgag 540  
agagacctca gcttttttagg aagaattcag ataactcatc attctatcga tggtcaccgc 600  
acgaattctg aaagcatgaa gaagtatgca gagcttgatt ttagttttat aaaaatccgg 660  
ctcttcaagg gaggatttct gtggcacagt cacactgttg aaattcaggg cctgtaacag 720  
ctcatcgata gctgtcagca tgttttgatc cagaaagatc tgcctcttgg gatccattaa 780  
aagctttgcg ttcattggcct tgaattccat ctggtacatc ttcaagtcct catagatgct 840  
gctaaggcac aggaccgtca taaaagaggc ctttccagag gccaggcaac tcccgttagt 900  
tatcaaagag atctctctgg aagccaggca actctcattc atggttaatt ccagtggtaa 960  
gcaggcctcc actgtgctgg ttttatcctt tgtgatatct tcatgatcaa tctcttcgga 1020  
agtgcaggaa tataattcta gagtttgtct ggccttctga agcgtgttgc tgacggctct 1080

cagcaggttt tgggagtggg tgaggcactg gaatattcct gggctcgggtg aggctgtggg 1140  
gaggctcctg gccaagtaa ggtgggtccag gtggcttagc aggaccagga tggtcacaag 1200  
gaggaggccg cgcggcgggc acatgctggg cgggcgctgc gtggaccccg gcgggcgctg 1260  
gacgcggaact gcggacgcgg caggggaggg cggcggtggg aggccgaccc ggggggtcac 1320  
atttttataa ttggcccgag gcgcgccagg actttcccg gactccgggtg tccggcttgc 1380  
tttctctctc tgtctctctc tacatcagct tctcggtgac acgtggagct gggcccgcgg 1440  
ggtttgccctc gtgcc 1455

<210> 107  
<211> 2267  
<212> DNA  
<213> Canis familiaris

<220>  
<221> CDS  
<222> (154) .. (1140)

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ggagtagggg atataagctc cagtagcagt agcagcagca gcaggagact ccgtttcaga 120  
cccagggaac cttgcagcct ggccagaagc aag atg cat cct cag cag ttg gtc 174  
Met His Pro Gln Gln Leu Val  
1 5  
atc tcc tgg ttt tcc ctc gtt ttg ctg gcg tct ccc ctc atg gcc ata 222  
Ile Ser Trp Phe Ser Leu Val Leu Leu Ala Ser Pro Leu Met Ala Ile  
10 15 20  
tgg gaa ctg gag aaa gat gtt tat gtt gta gag ttg gac tgg cac cct 270  
Trp Glu Leu Glu Lys Asp Val Tyr Val Val Glu Leu Asp Trp His Pro  
25 30 35  
gat gcc ccc gga gaa atg gtg gtc ctc acc tgc cat acc cct gaa gaa 318  
Asp Ala Pro Gly Glu Met Val Val Leu Thr Cys His Thr Pro Glu Glu  
40 45 50 55  
gat gac atc act tgg acc tca gcg cag agc agt gaa gtc cta ggt tct 366  
Asp Asp Ile Thr Trp Thr Ser Ala Gln Ser Ser Glu Val Leu Gly Ser  
60 65 70  
ggt aaa act ctg acc atc caa gtc aaa gaa ttt gga gat gct ggc cag 414  
Gly Lys Thr Leu Thr Ile Gln Val Lys Glu Phe Gly Asp Ala Gly Gln  
75 80 85  
tat acc tgc cat aaa gga ggc aag gtt ctg agc cgc tca ctc ctg ttg 462  
Tyr Thr Cys His Lys Gly Gly Lys Val Leu Ser Arg Ser Leu Leu Leu

90	95	100	
att cac aaa aaa gaa gat gga att tgg tcc act gat atc tta aag gaa Ile His Lys Lys Glu Asp Gly Ile Trp Ser Thr Asp Ile Leu Lys Glu 105 110 115			510
cag aaa gaa tcc aaa aat aag atc ttt ctg aaa tgt gag gca aag aat Gln Lys Glu Ser Lys Asn Lys Ile Phe Leu Lys Cys Glu Ala Lys Asn 120 125 130 135			558
tat tct gga cgt ttc aca tgc tgg tgg ctg acg gca atc agt act gat Tyr Ser Gly Arg Phe Thr Cys Trp Trp Leu Thr Ala Ile Ser Thr Asp 140 145 150			606
ttg aaa ttc agt gtc aaa agt agc aga ggc ttc tct gac ccc caa ggg Leu Lys Phe Ser Val Lys Ser Ser Arg Gly Phe Ser Asp Pro Gln Gly 155 160 165			654
gtg aca tgt gga gca gtg aca ctt tca gca gag agg gtc aga gtg gac Val Thr Cys Gly Ala Val Thr Leu Ser Ala Glu Arg Val Arg Val Asp 170 175 180			702
aac agg gat tat aag aag tac aca gtg gag tgt cag gag ggc agt gcc Asn Arg Asp Tyr Lys Lys Tyr Thr Val Glu Cys Gln Glu Gly Ser Ala 185 190 195			750
tgc ccc tct gcc gag gag agc cta ccc atc gag gtc gtg gtg gat gct Cys Pro Ser Ala Glu Glu Ser Leu Pro Ile Glu Val Val Val Asp Ala 200 205 210 215			798
att cac aag ctc aag tat gaa aac tac acc agc agc ttc ttc atc aga Ile His Lys Leu Lys Tyr Glu Asn Tyr Thr Ser Ser Phe Phe Ile Arg 220 225 230			846
gac atc atc aaa cca gac cca ccc aca aac ctg cag ctg aag cca ttg Asp Ile Ile Lys Pro Asp Pro Pro Thr Asn Leu Gln Leu Lys Pro Leu 235 240 245			894
aaa aat tct cgg cac gtg gag gtc agc tgg gaa tac ccc gac acc tgg Lys Asn Ser Arg His Val Glu Val Ser Trp Glu Tyr Pro Asp Thr Trp 250 255 260			942
agc acc cca cat tcc tac ttc tcc ctg aca ttt tgc ata cag gcc cag Ser Thr Pro His Ser Tyr Phe Ser Leu Thr Phe Cys Ile Gln Ala Gln 265 270 275			990
ggc aag aac aat aga gaa aag aaa gat aga ctc tgc gtg gac aag acc Gly Lys Asn Asn Arg Glu Lys Lys Asp Arg Leu Cys Val Asp Lys Thr 280 285 290 295			1038
tca gcc aag gtc gtg tgc cac aag gat gcc aag atc cgc gtg caa gcc Ser Ala Lys Val Val Cys His Lys Asp Ala Lys Ile Arg Val Gln Ala 300 305 310			1086
cga gac cgc tac tat agt tca tcc tgg agc gac tgg gca tct gtg tcc Arg Asp Arg Tyr Tyr Ser Ser Ser Trp Ser Asp Trp Ala Ser Val Ser 315 320 325			1134

tgc agt taggttccac ccccaggatg aatcttggag ggaaagtgga agatattatg 1190  
Cys Ser

caaaattttc taaggacaca ttgaagagge tccaaaagtt attttctgcc taattttctt 1250  
tttgtaaagg gtcattattg tgtcttcgca atatttttta catttaaag ccaaagcccc 1310  
actgaaacaa tcagctactt tatttataga ttttcagcta gcaggctgcc actgacctta 1370  
atgctattta aatatttaag taatttatgt atttattaat ttattgttat tgaacacttg 1430  
tgtgccaaga tatattgtat gtttcatacc ctccaggacct gatctgtaag gaataggccc 1490  
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<211> 329

<212> PRT

<213> Canis familiaris

<400> 108

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Val Glu Leu Asp Trp His Pro Asp Ala Pro Gly Glu Met Val Val Leu  
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Thr Cys His Thr Pro Glu Glu Asp Asp Ile Thr Trp Thr Ser Ala Gln  
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Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys  
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Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Lys Val  
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Leu Ser Arg Ser Leu Leu Leu Ile His Lys Lys Glu Asp Gly Ile Trp  
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Ser Thr Asp Ile Leu Lys Glu Gln Lys Glu Ser Lys Asn Lys Ile Phe  
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Leu Lys Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp  
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Leu Thr Ala Ile Ser Thr Asp Leu Lys Phe Ser Val Lys Ser Ser Arg  
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Gly Phe Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Val Thr Leu Ser  
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Ala Glu Arg Val Arg Val Asp Asn Arg Asp Tyr Lys Lys Tyr Thr Val  
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Glu Cys Gln Glu Gly Ser Ala Cys Pro Ser Ala Glu Glu Ser Leu Pro  
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Ile Glu Val Val Val Asp Ala Ile His Lys Leu Lys Tyr Glu Asn Tyr  
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Thr Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Thr  
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Asn Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg His Val Glu Val Ser  
 245 250 255

Trp Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu

260

265

270

Thr Phe Cys Ile Gln Ala Gln Gly Lys Asn Asn Arg Glu Lys Lys Asp  
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Arg Leu Cys Val Asp Lys Thr Ser Ala Lys Val Val Cys His Lys Asp  
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Ser Asp Trp Ala Ser Val Ser Cys Ser  
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<210> 111  
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